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(54) Title: CONJUGATES OF VASCULAR ENDOTHELIAL GROWTH FACTOR WITH TARGETED AGENTS

(57) Abstract

Conjugates of vascular endothelial growth factor (VEGF) linked, either directly or via a linker, to a targeted agent are provided. The targeted agent is a cytotoxic agent, such as a ribosome-inactivating protein (RIP) and an antisense nucleic acid, or is a therapeutic nucleic acid for targeted delivery to vascular endothelial cells. The targeted agent is attached to VEGF, or via a linker, through a chemical bond, or the conjugate is prepared as a chimera using techniques of recombinant DNA. The conjugates are used to target cytotoxic agents or therapeutic nucleotides to endothelial cells and are particularly useful for treating solid tumors, such as Kaposi's sarcoma, and for treating ophthalmic disorders with underlying vascular proliferation.

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Description

**CONJUGATES OF VASCULAR ENDOTHELIAL
GROWTH FACTOR WITH TARGETED AGENTS**

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Technical Field

The present invention relates to the treatment of diseases, and more specifically, to the preparation of conjugates of a vascular endothelial cell growth factor and a targeted agent, and their use in altering the function, gene-expression, or viability of a cell in a therapeutic manner.

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Background of the Invention

A major goal of treatment of neoplastic diseases and hyperproliferative disorders is to ablate the abnormally growing cells while leaving normal cells untouched. Various methods are under development for providing treatment, but none provide the requisite degree of specificity.

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One method of treatment is to deliver toxins to appropriate targets. Immunotoxins and cytotoxins are protein conjugates of toxin molecules with either antibodies or factors which bind to receptors on target cells. Three major problems may limit the usefulness of immunotoxins. First, the antibodies may react with more than one cell surface molecule, thereby effecting delivery to multiple cell types, possibly including normal cells. Second, even if the antibody is specific, the antibody reactive molecule may be present on normal cells. Third, the toxin molecule may be toxic to cells prior to delivery and internalization. Cytotoxins suffer from similar disadvantages of specificity and toxicity. Another limitation in the therapeutic use of immunotoxins and cytotoxins is the relatively low ratio of therapeutic to toxic dosage. Additionally, it may be difficult to direct sufficient concentrations of the toxin into the cytoplasm and intracellular compartments in which the agent can exert its desired activity.

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Given these limitations, cytotoxic therapy has been attempted using viral vectors to deliver DNA encoding the toxins into cells. If eukaryotic viruses are used, such as the retroviruses currently in use, they may recombine with host DNA to produce infectious virus. Moreover, because retroviral vectors are often inactivated by the complement system, use *in vivo* is limited. Retroviral vectors also lack specificity in delivery; receptors for most viral vectors are present on a large fraction, if not all, cells. Thus, infection with such a viral vector will infect normal as well as abnormal

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cells. Because of this general infection mechanism, it is not desirable for a viral vector to directly encode a cytotoxic molecule.

While delivery of nucleic acids offers advantages over delivery of cytotoxic proteins such as reduced toxicity prior to internalization, there is a need for high specificity of delivery, which is currently unavailable with the present systems.

In view of the problems associated with gene therapy, there is a compelling need for improved treatments which are more effective and are not associated with such disadvantages. The present invention exploits the use of conjugates which have increased specificity and deliver higher amounts of nucleic acids to targeted cells, while providing other related advantages.

Summary of the Invention

The present invention generally provides conjugates of vascular endothelial cell growth factor (VEGF) polypeptide or a portion thereof and a targeted agent. In one embodiment of this invention, the VEGF and targeted agent are conjugated through a linker. Within each conjugate, there can be more than one VEGF and targeted agent molecule. Preferably, in the conjugates, there are between one and six VEGF and targeted agents, and most preferably one VEGF molecule and one targeted agent conjugated prior to dimerization. In certain embodiments, the linker is selected from the group consisting of protease substrates, linkers that increase the flexibility of the conjugate, linkers that increase the solubility of the conjugate, photocleavable linkers and acid cleavable linkers. In certain other embodiments, the VEGF polypeptide may be native human or bovine VEGF or VEGF, which is modified by addition of a cysteine residue or replacement of a nonessential amino acid residue within about 20 amino acids of the N-terminus or C-terminus. In yet other embodiments, the targeted agent is cytotoxic, preferably a ribosome inactivating protein, and most preferably saporin. Other cytotoxic agents include methotrexate, anthracyclines, *Pseudomonas* exotoxin, porphyrin, or a nucleic acid.

In another embodiment, the conjugate has the formula: targeted agent-(L)_q-VEGF-(L)_r-VEGF, wherein q and r, which may be the same or different, are 0 or 1. In yet another embodiment, the conjugate has the formula: targeted agent-(L)_q-VEGF.

In other aspects, methods of targeting an agent to cells bearing VEGF receptors, comprises conjugating the targeted agent to one or more VEGF monomers or portions thereof that bind to a VEGF receptor, whereby the conjugated targeted agent is internalized by the cells. In another aspect, methods of treating VEGF-mediated pathophysiological conditions, comprising administering to the animal a therapeutically

effective amount of a conjugate between VEGF and a cytotoxic agent, are provided. In certain embodiments, the condition is a dermatological disorder with underlying vascular proliferation, a solid tumor, or an ophthalmic disorder, such as diabetic retinopathy, proliferative vitreoretinopathy, and pterygium. The dermatological disorder is Kaposi's sarcoma, psoriasis or macular degeneration. Methods are also provided to inhibit proliferation of cells bearing VEGF receptors, comprising contacting the cells with an effective amount of a VEGF targeted agent conjugate.

In yet other aspects, methods of effecting gene therapy are provided, wherein cells are contacted with a conjugate having a targeted agent which is a nucleic acid, and the conjugate includes a nuclear translocation sequence linked to the targeted nucleic acid or VEGF.

In yet other aspects, DNA fragments, encoding a conjugate between a targeted agent and VEGF are provided. In certain embodiments, the DNA conjugate may additionally comprise a linker. Plasmids, vectors, and host cells are also provided. In another embodiment, methods of producing conjugate of VEGF and a targeted agent comprising growing a culture of cells transformed with a vector containing a VEGF cytotoxic agent conjugate whereby DNA is transcribed and translated to produce the conjugate are provided.

In other embodiments, the VEGF monomer that is modified by insertion of a cysteine residue within about 20 amino acids of the N-terminus or C-terminus, wherein the inserted residue replaces a nonessential residue in the unmodified VEGF monomer is provided.

Pharmaceutical compositions, comprising the VEGF targeted agent conjugate and a physiological acceptable excipient are also provided.

These and other aspects of the present invention will become evident upon reference to the following detailed description and attached drawings. In addition, various references are set forth below which describe in more detail certain procedures or compositions, and are therefore incorporated by reference in their entirety.

Brief Description of the Drawings

Figure 1 is a Coomassie blue stained polyacrylamide-SDS gel and Western blot analyses of VEGF production using the pP_L-λ expression system. Inclusion bodies were isolated from bacteria by the addition of lysozyme followed by centrifugation. Equal amounts of each sample were run under reducing conditions. An antibody to an N-terminus peptide of VEGF (Oncogene Sciences) was used in the Western analysis. Lanes 1 and 5, VEGF₁₆₅ t=0 hours post-induction; lanes 3 and 7, VEGF₁₂₁ t=0 hours post-induction; lanes 2 and 6, VEGF₁₆₅ t=2 hours post-induction;

lanes 4 and 8, VEGF₁₂₁ t=2 hours post-induction. Proteins of expected molecular weights of 19.2 kD for monomeric VEGF₁₆₅ and 14.2kD for monomeric VEGF₁₂₁ were observed.

Figure 2 is a Coomassie blue stained polyacrylamide-SDS gel analysis of VEGF₁₂₁ and VEGF₁₆₅ under reducing and non-reducing conditions. Inclusion bodies were isolated and VEGF refolded and dimerized under the given conditions. Lanes 1 and 3, VEGF₁₂₁; lanes 2 and 4, VEGF₁₆₅. The predicted molecular weights for VEGF₁₂₁ are 14.2 kD and 28.4 kD for monomeric and dimeric forms respectively. The predicted molecular weights for VEGF₁₆₅ are 19.2 kD and 38.4 kD for monomeric and dimeric forms respectively.

Figure 3 is a graph of the results of an acid phosphate assay, which measures viable cell members, showing that purified VEGF₁₂₁ or VEGF₁₆₅ made in *E. coli* can stimulate proliferation of HMVEC (human microvascular endothelial cells). VEGF₁₂₁ and VEGF₁₆₅ were isolated from inclusion bodies and tested for their ability to induce proliferation of HMVEC. *E. coli* derived material is shown in comparison to either VEGF₁₂₁ or VEGF₁₆₅ produced in insect cells (R&D, BV). Both forms of VEGF produced in *E. coli* induce proliferation of HMVEC in a dose dependent manner at concentrations as low as 10⁻¹¹ to 10⁻¹⁰M. VEGF₁₂₁ produced in *E. coli* is more potent than VEGF₁₂₁ produced in insect cells, while VEGF₁₆₅ made in *E. coli* is less active.

Figure 4 is a Coomassie blue stained polyacrylamide-SDS gel and Western blot analysis of VEGF-SAP mitotoxin production using the pP_L-λ expression system. Inclusion bodies were isolated from bacteria by the addition of lysozyme followed by centrifugation. Equal amounts of each sample were run under reducing conditions. An antibody to an N-terminus peptide of saporin was used in the Western analysis. Lanes 1 and 3, VEGF₁₂₁-SAP; lanes 2 and 4, VEGF₁₆₅-SAP. Proteins of expected molecular weights of 42.2 kD for VEGF₁₂₁-SAP and 47.2 kD for VEGF₁₆₅-SAP were observed.

Figure 5 is a Coomassie blue stained polyacrylamide-SDS gel of VEGF₁₂₁-SAP run under reducing and non-reducing conditions. Inclusion bodies were isolated and VEGF₁₂₁-SAP refolded under the given conditions. The predicted molecular weight for VEGF₁₂₁-SAP is 42.2 kD under reducing conditions.

Figure 6 is a graph depicting inhibition of protein synthesis in a cell-free system. The effect of VEGF₁₂₁-SAP on protein synthesis in a cell-free luciferase system was compared to that of SAP.

Figure 7 is a graph showing that VEGF₁₆₅-SAP inhibits proliferation of HMVEC (human microvascular endothelial cells) in a dose dependent manner. CCSV.

chemical conjugate VEGF₁₆₅-SAP; FPSV, SAP-VEGF₁₂₁ made in *E. coli* from inclusion bodies; VEGF₁₂₁, insect cell derived.

Detailed Description of the Invention

5 Definitions

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as is commonly understood by one of skill in the art to which the subject matter herein belongs.

10 The "amino acids" are identified according to their well-known, three-letter or one-letter abbreviations. The nucleotides, which occur in the various DNA fragments, are designated with the standard single-letter designations used routinely in the art.

As used herein, to "bind to a receptor" refers to the ability of VEGF to detectably bind to such receptors as assayed by standard *in vitro* assays. For example,
15 binding measures the capacity of a VEGF conjugate, VEGF monomer, or VEGF dimer to recognize the VEGF receptor on vascular endothelial cells, such as an aortic vascular endothelial cell line using a procedure such as the one described in Moscatelli (*J. Cell Physiol.* 131:123-130, 1987). Briefly, cells are grown to subconfluence and incubated in appropriate buffer with radioiodinated VEGF dimer in the presence of various
20 concentrations of the VEGF monomer or dimer or VEGF conjugate of interest. Binding affinity is measured by counting the membrane fraction that is solubilized in a suitable buffer containing a detergent, such as in 0.5% Triton X-100 in PBS (pH 8.1).

As used herein, "biological activity" refers to the *in vivo* activities of a compound or physiological responses that result upon *in vivo* administration of a
25 compound, composition or other mixture. Biological activity, thus, encompasses therapeutic effects and pharmaceutical activity of such compounds, compositions and mixtures. Such biological activity may, however, be defined with reference to particular *in vitro* activities, as measured in a defined assay. Thus, for example, reference herein to the biological activity or reactivity of VEGF, a dimer thereof,
30 monomer, or fragment thereof, or other combination of VEGF monomers and fragments, refers to the ability of the VEGF to bind to cells bearing VEGF receptors and internalize a linked agent. Such activity is typically assessed *in vitro* by linking the VEGF (dimer, monomer or fragment) to a cytotoxic agent, such as saporin, contacting cells bearing VEGF receptors, such as aortic endothelial cells, with the conjugate and
35 assessing cell proliferation or growth. *In vivo* activity may be assessed using recognized animal models, such as the mouse xenograft model for anti-tumor activity (see, e.g., Beitz et al. (1992) *Cancer Research* 52:227-230; Houghton et al. (1982)

Cancer Res. 42:535-539; Bogden et al. (1981) *Cancer (Philadelphia)* 48:10-20; Hoogenhout et al. (1983) *Int. J. Radiat. Oncol., Biol. Phys.* 9:871-879; Stastny et al. (1993) *Cancer Res.* 53:5740-5744).

As used herein, a "conjugate" refers to a molecule that contains at least one VEGF moiety and at least one targeted agent that are linked directly or via a linker and that are produced by chemical coupling methods or by recombinant expression of chimeric DNA molecules to produce fusion proteins.

As used herein, the term "cytotoxic agent" refers to a molecule capable of inhibiting cell function. The agent may inhibit cell growth, differentiation or proliferation or be toxic to cells. The term includes agents whose toxic effects are mediated only when transported into the cell and also those whose toxic effect is mediated at the cell surface. A variety of cytotoxic agents can be used and include those that inhibit protein synthesis and those that inhibit expression of certain genes essential for cell growth or survival.

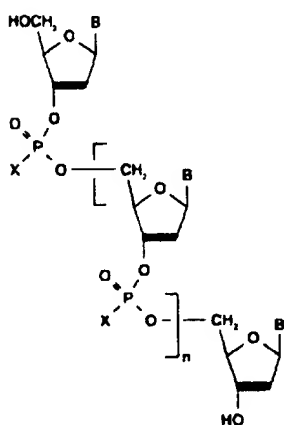
As used herein, "DNA encoding a VEGF peptide or polypeptide" refers to any of the DNA fragments set forth herein as coding such peptides, to any such DNA fragments known to those of skill in the art, any DNA fragment that encodes a VEGF that binds to a VEGF receptor and is internalized thereby. Such a DNA molecule may be isolated from a human cell library using any DNA fragment that encodes any of the VEGF peptides set forth in SEQ ID NOs. 25-28 or any DNA fragment that may be produced from any of the preceding DNA fragments by substitution of degenerate codons. It is understood that once the complete amino acid sequence of a peptide, such as a VEGF peptide, is available to those of skill in this art, it is routine to substitute degenerate codons and produce any of the possible DNA fragments that encode such peptide. It is also generally possible to synthesize DNA encoding such peptide based on the amino acid sequence.

As used herein, a "fusion protein" refers to a polypeptide that contains at least two components, such as VEGF and a targeted agent or VEGF and linker, and is produced by expression of DNA in a host cell.

As used herein, "nucleic acids" refer to RNA or DNA that are intended as targeted agents, which include, but are not limited to, DNA encoding therapeutic proteins, fragments of DNA for co-suppression, DNA encoding cytotoxic proteins, antisense nucleic acids and other such molecules. Reference to nucleic acids includes duplex DNA, single-stranded DNA, RNA in any form, including triplex, duplex or single-stranded RNA, anti-sense RNA, polynucleotides, oligonucleotides, single nucleotides and derivatives thereof.

Nucleic acids may be composed of the well-known deoxyribonucleotides or ribonucleotides composed of the bases: adenosine, cytosine, guanine, thymidine, and uridine. As well, various other nucleotide derivatives and non-phosphate backbones or phosphate derivative backbones may be used.

5 For example, because normal phosphodiester oligonucleotides (referred to as PO oligonucleotides or type I; see structure, below, where X = O) are sensitive to DNA- and RNA-specific nucleases, several resistant types of oligonucleotides have been developed (*see, e.g.*, International Application WO 93/23570, which is based on 07/881,255, filed May 11, 1992; International Application WO 93/15742, which is
10 based on 07/833,146, filed February 10, 1992; Wagner et al. (1993) *Science* 260:1510-1514; U.S. Patent No. 5,218,088, U.S. Patent No. 5,175,269; U.S. Patent No. 5,109,124; Carter et al. (1993) *Br. J. Cancer* 67:869-876); these include types II-IV:



in which B is a nucleotide base; and X is OEt in phosphotriester (type II), X is Me in methylphosphonate (type III; referred to as MP oligos); and X is S in phosphorothioate (referred to as PS oligos; U.S. Patent No. 5,218,088 to Gorenstein et al. describes a method for preparation of PS oligos). Presently, MP and PS oligonucleotides have been the focus of most investigation.

As used herein, the term "VEGF" refers to any polypeptide that, either as a monomer or dimer, binds to a VEGF receptor and is transported into the cell by virtue of its interaction with the receptor. A polypeptide that is "reactive" with the receptor
25 binds to the receptor and is internalized. VEGF refers to peptides having amino acid sequences of native VEGF polypeptide monomers, as well as VEGF polypeptides modified by amino acid substitutions, deletions, insertions or additions in the native protein, but alone or linked to a targeted agent retains the ability to bind to a VEGF receptor and to be internalized in a cell bearing such receptor. Such polypeptides
30 include, but are not limited to human VEGF₁₂₁, human VEGF₁₆₅, human VEGF₁₈₉, human VEGF₂₀₆, bovine VEGF₁₂₀, bovine VEGF₁₆₄, bovine VEGF₁₈₈, bovine VEGF₂₀₅, and homodimers and heterodimers of any VEGF monomer or monomers. In addition, peptides reactive with VEGF receptors that are isolated by phage display (U.S. Patent No. 5,223,409 and 5,403,484) are encompassed as well. It is understood
35 that differences in amino acid sequences can occur among VEGFs of different species as well as among VEGFs from individual organisms or species and that such minor allelic variations or variations among species are intended to be encompassed by

reference to VEGF herein. As used herein a "portion of a VEGF" refers to a fragment or piece of VEGF that is sufficient, either alone or as a dimer with another fragment or a VEGF polypeptide, to bind to a VEGF receptor and internalize a linked targeted agent.

5 Muteins of VEGF include, but are not limited to, those produced by replacing one or more of the cysteines with serine as herein or those that have any other amino acids deleted or replaced. Typically, muteins will have conservative amino acid changes, such as those set forth below in Table 1. DNA encoding such muteins will, unless modified by replacement of degenerate codons, hybridize under conditions of at
10 least low stringency to DNA encoding a VEGF (SEQ ID NOs. 25-28) or an exon thereof (SEQ ID NOs. 16-24). VEGF may be isolated from natural sources or be made synthetically, such as by recombinant means or chemical synthesis.

As used herein, "VEGF-mediated pathophysiological condition" refers to a deleterious condition characterized by or caused by proliferation of cells that are
15 sensitive to VEGF mitogenic stimulation.

As used herein, "VEGF receptors" refer to receptors that react with a naturally-occurring member of the VEGF family of proteins and transport it into a cell bearing such receptors. Included among these are the *fms*-like tyrosine kinase receptor (FLT) and the kinase insert domain-containing receptor (KDR) (*see, e.g.*, International
20 Application WO 92/14748, which is based on U.S. Applications Serial No. 08/657,236, de Vries et al. (1992) *Science* 255:989-91; Terman et al. (1992) *Biochem. Biophys. Res. Commun.* 187:1579-1586; Kendall et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:10705-10709; and Peters et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8915-8919).

As used herein, a "targeted agent" is any agent that is intended for
25 internalization by linkage to VEGF, and that upon internalization alters or affects cellular metabolism, growth, activity, viability or other property or characteristic of the cell. The targeted agents include proteins, polypeptides, organic molecules, drugs, nucleic acids and other such molecules. As used herein, to target a targeted agent, such as a cytotoxic agent, means to direct it to a cell that expresses a selected receptor by
30 linking the agent to a polypeptide reactive with a VEGF receptor.

As used herein, a "therapeutic nucleic acid" describes any nucleic acid used in the contest of invention that modify gene transcription or translation. This term also includes nucleic acids that bind to sites on proteins and to receptors. It includes, but is not limited to the following types of nucleic acids: nucleic acids encoding a
35 protein, antisense RNA, DNA intended to form triplex molecules, extracellular protein binding oligonucleotides and small nucleotide molecules. A therapeutic nucleic acid may serve as a replacement for a defective gene or encode a therapeutic product, such

as TNF or a cytotoxic molecule, such as saporin. The therapeutic nucleic acid may encode all or a portion of a gene, and may function by recombining with DNA already present in a cell, thereby replacing a defective portion of a gene. It may also encode a portion of a protein and exert its effect by virtue of co-suppression of a gene product.

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A. Vascular endothelial growth factors

1. Polypeptides reactive with a VEGF receptor

Vascular endothelial growth factors (VEGFs) were identified by their ability to directly stimulate endothelial cell growth, but do not appear to have mitogenic effects on other types of cells. VEGFs also cause a rapid and reversible increase in blood vessel permeability. The members of this family have been referred to variously as vascular endothelial growth factor (VEGF), vascular permeability factor (VPF) and vasculotropin (*see, e.g., Plouet et al., EMBO J. 8:3801-3806, 1989*). Herein, they are collectively referred to as VEGF.

VEGF was originally isolated from a guinea pig hepatocarcinoma cell line, line 10, (*see, e.g., U.S. Patent No. 4,456,550*) and has subsequently been identified in humans and in normal cells. It is expressed during normal development and in certain normal adult organs. Purified VEGF is a basic, heparin-binding, homodimeric glycoprotein that is heat-stable, acid-stable and may be inactivated by reducing agents.

DNA sequences encoding VEGF and methods to isolate these sequences may be found primarily in U.S. Patent No. 5,240,848, U.S. Patent No. 5,332,671, U.S. Patent No. 5,219,739, U.S. Patent No. 5,194,596, and Houch et al., *Mol. Endocrin.* 5:180, 1991.

VEGF family members arise from a single gene organized as eight exons and spanning approximately 14 kb in the human genome. Four molecular species of VEGF result from alternative splicing of mRNA and contain 121, 165, 189 and 206 amino acids. The four species have similar biological activities, but differ markedly in their secretion patterns. The predominant isoform secreted by a variety of normal and transformed cells is VEGF₁₆₅. Transcripts encoding VEGF₁₂₁ and VEGF₁₈₉ are detectable in most cells and tissues that express the VEGF gene. In contrast, VEGF₂₀₆ is less abundant and has been identified only in a human fetal liver cDNA library. VEGF₁₂₁ is a weakly acidic polypeptide that lacks the heparin binding domain and, consequently, does not bind to heparin. VEGF₁₈₉ and VEGF₂₀₆ are more basic than VEGF₁₆₅ and bind to heparin with greater affinity. Although not every identified VEGF isoform binds heparin, all isoforms are considered to be heparin-binding growth factors within the context of this invention.

The secreted isoforms, VEGF₁₂₁ and VEGF₁₆₅ are preferred VEGF proteins. VEGF₁₂₁ is particularly preferred. The longer isoforms, VEGF₁₈₉ and VEGF₂₀₆, are almost completely bound to the extracellular matrix and need to be released by an agent, such as urokinase, suramin, heparin or heparinase, and plasmin.

5 Other preferred VEGF proteins contain various combinations of VEGF exons, such that the protein still binds VEGF receptor and is internalized. It is not necessary that a VEGF protein used in the context of this invention either retain any of its *in vivo* biological activities, such as stimulating endothelial cell growth, or bind heparin. It is only necessary that the VEGF protein or fragment thereof bind the VEGF receptor and

10 be internalized into the cell bearing the receptor. However, it may be desirable in certain contexts for VEGF to manifest certain of its biological activities. For example, if VEGF is used as a carrier for DNA encoding a molecule useful in wound healing, it would be desirable that VEGF exhibit vessel permeability activity and promotion of fibroblast migration and angiogenesis. It will be apparent from the teachings provided

15 within the subject application which of the activities of VEGF are desirable to maintain.

VEGF promotes an array of responses in endothelium, including blood vessel hyperpermeability, endothelial cell growth, angiogenesis, cell migration and enhanced glucose transport. VEGF stimulates the growth of endothelial cells from a variety of sources (including brain capillaries, fetal and adult aortas, and umbilical

20 veins) at low concentrations, but is reported to have no effect on the growth of vascular smooth muscle cells, adrenal cortex cells, keratinocytes, lens epithelial cells, or BHK-21 fibroblasts. VEGF also is a potent polypeptide regulator of blood vessel function; it causes a rapid but transient increase in microvascular permeability without causing endothelial cell damage or mast cell degranulation, and its action is not blocked by

25 antihistamines. VEGF has also been reported to induce monocyte migration and activation and has been implicated as a tumor angiogenesis factor in some human gliomas. Also, VEGF is a chemoattractant for monocytes and VEGF has been shown to enhance the activity of the inflammatory mediator tumor necrosis factor (TNF).

Quiescent and proliferating endothelial cells display high-affinity

30 binding to VEGF, and endothelial cell responses to VEGF appear to be mediated by high affinity cell surface receptors. Two tyrosine kinases have been identified as VEGF receptors. The first, known as fms-like tyrosine kinase or FLT is a receptor tyrosine kinase that is specific for VEGF. In adult and embryonic tissues, expression of FLT mRNA is localized to the endothelium and to populations of cells that give rise to

35 endothelium. The second receptor KDR (human kinase insert domain-containing receptor), and its mouse homologue FLK-1, are closely related to FLT. The KDR/FLK-1 receptor is expressed in endothelium during the fetal growth stage, during

earlier embryonic development, and in adult tissues. In addition, messenger RNA encoding FLT and KDR have been identified in tumor blood vessels and specifically by endothelial cells of blood vessels supplying glioblastomas. Similarly, FLT and KDR mRNAs are upregulated in tumor blood vessels in invasive human colon
5 adenocarcinoma, but not in the blood vessels of adjacent normal tissues.

VEGF suitable for use herein also includes any polypeptide or fragment of a VEGF protein that retains the ability, either as a monomer or as part of a dimer, to bind to a VEGF receptor and to be internalized by a cell bearing such receptor. In addition, VEGF include any combination of peptides encoded by the exons set forth in
10 SEQ ID NOs. 16-24 that retains the requisite receptor binding and internalization activities. Amino acid sequence variations in VEGF, including allelic variations and conservative amino acid substitutions, such as those set forth in TABLE 1, that do not alter its ability to bind to VEGF receptors and to be internalized by cells upon such binding are suitable for use in the present invention.

The various VEGF isoforms that result from alternative splicing of RNA transcribed from a VEGF gene (*see, e.g.*, U.S. Patent No. 5,219,739 to Tischer et al.; U.S. Patent No. 5,194,596 to Tisher et al.; U.S. Patent No. 5,240,848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications
15 nos. 07/351,361, 07/369,424, 07/389,722, to Genentech, Inc., and U.S. applications Serial Nos. 07/351,361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 A1 and EP 0 476 983 A1 to Merck & Co.; Houck et al. (1991) *Mol. Endo.* 5:1806-1814; *see also* SEQ ID NOs. 18-28; *see, also* SEQ ID Nos. 86-89, for modified forms produced herein) are also suitable for use in the present invention.

Any polypeptide that is reactive with a VEGF receptor may be used in
25 the present invention. VEGF conjugates preferably include at least two VEGF monomers in an antiparallel orientation. Dimer formation occurs when VEGF monomers are mixed under physiological or other appropriate conditions. Also, expression of tandem repeats of VEGF as fusion proteins, with or without linkers separating the monomers, should result in dimers upon expression of DNA encoding
30 the VEGF fusion proteins.

VEGF may be isolated from any mammalian source, including human, bovine and murine sources, although human is preferred. The VEGF polypeptides include those that, when dimerized, are mitogenic to vascular endothelial cells. Mitogenic activity, however, is not required for the VEGF moieties used herein. It is
35 sufficient that the polypeptide, bind to a VEGF receptor and internalize a linked agent.

2. Modifications of VEGF

The preferred VEGF molecules are those that are set forth in SEQ ID Nos. 25-28 or peptides that have minor sequence variations of the peptides. Such minor sequence variations include, but are not limited to, minor allelic or species variations and insertions or deletions of residues, particularly cysteine residues. Suitable conservative substitutions of amino acids are known to those of skill in this art and may be made generally without altering the biological activity of the resulting molecule. Those of skill in this art recognize that, in general, single amino acid substitutions in non-essential regions of a polypeptide do not substantially alter biological activity (*see, e.g., Watson et al. Molecular Biology of the Gene*, 4th Edition, 1987, The Benjamin/Cummings Pub. Co., p.224). Such substitutions are preferably made in accordance with those set forth in TABLE 1 as follows:

TABLE 1

Original Residue	Conservative substitution
Ala (A)	Gly; Ser
Arg (R)	Lys
Asn (N)	Gln; His
Cys (C)	Ser; neutral amino acid
Gln (Q)	Asn
Glu (E)	Asp
Gly (G)	Ala; Pro
His (H)	Asn; Gln
Ile (I)	Leu; Val
Leu (L)	Ile; Val
Lys (K)	Arg; Gln; Glu
Met (M)	Leu; Tyr; Ile
Phe (F)	Met; Leu; Tyr
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Tyr
Tyr (Y)	Trp; Phe
Val (V)	Ile; Leu

Other substitutions are also permissible and may be determined empirically or in accord with known conservative substitutions. Any such modification of the polypeptide may be effected by any means known to those of skill in this art.

VEGF peptides include those having SEQ ID NOs. 25-28, and versions thereof that lack the leader sequence (amino acids 1-26 in any of SEQ ID NOs. 25-28), including VEGF precursors that include all or a part of the signal sequence, or modified forms of VEGF that retain the requisite activities (the ability to bind to a VEGF receptor and internalize a linked targeted agent). Members of the VEGF protein family, including human VEGF₁₂₁, human VEGF₁₆₅, human VEGF₁₈₉, human VEGF₂₀₆, are preferred. VEGF₁₂₁ is particularly preferred. As provided herein VEGF₁₂₁ has SEQ ID NO. 25, see, also SEQ ID NOs. 86 and 88 for modified forms, and also is formed from EXONS I-V and VIII (SEQ ID NOs. 16-20 and 24); VEGF₁₆₅ has SEQ ID NO. 26, see, also SEQ ID NOs. 87 and 89 for modified forms, and also is formed from EXONS I-V, VII and VIII (SEQ ID NOs. 16-20, 23 and 24); VEGF₁₈₉ has SEQ ID NO. 27, and also is formed from EXONS I-VII and VIII (SEQ ID NOs. 16-21, 23 and 24); and VEGF₂₀₆ has SEQ ID NO. 28, and also is formed from EXONS I-VI, the insert between EXONS VI and VII (see, SEQ ID NO. 22), and EXONS VII and VIII (SEQ ID NOs. 16-24). It is noted that in the sequence of EXON V SEQ ID NO. 2, the second Lys-encoding codon AAG, has been reported as AAA. Consequently, in the VEGF 165, 189, and 206 forms, which contain this codon, the sequence, reported here with the AAG codon, can also be AAA. Molecules, synthetic or naturally occurring, that may be formed from combinations of SEQ ID NOs. 16-24 (or allelic or minor conservatively substituted variations thereof) that possess the ability to bind to a VEGF receptor and internalize a linked targeted agent are intended for use herein. If necessary, such combinations of exons may be identified empirically by synthesizing the molecule and testing it, using assays described herein or any other assays known to those of skill in this art, for the ability, either as a monomer, or preferably as a dimer, to bind to a VEGF receptor and internalize a linked targeted agent.

Mutation may be effected by any method known to those of skill in the art, including site-specific or site-directed mutagenesis of DNA encoding the protein and the use of DNA amplification methods using primers to introduce and amplify alterations in the DNA template, such as PCR splicing by overlap extension (SOE). Site-specific mutagenesis is typically effected using a phage vector that has single- and double-stranded forms, such as M13 phage vectors, which are well-known and commercially available. Other suitable vectors that contain a single-stranded phage origin of replication may be used (*see, e.g., Veira et al. (1987) Meth. Enzymol. 15:3*). In general, site-directed mutagenesis is performed by preparing a single-stranded vector

that encodes the protein of interest (*i.e.*, a member of the VEGF family or a cytotoxic molecule, such as a saporin). An oligonucleotide primer that contains the desired mutation within a region of homology to the DNA in the single-stranded vector is annealed to the vector followed by addition of a DNA polymerase, such as *E. coli* polymerase I Klenow fragment, which uses the double stranded region as a primer to produce a heteroduplex in which one strand encodes the altered sequence and the other the original sequence. The heteroduplex is introduced into appropriate bacterial cells and clones that include the desired mutation are selected. The resulting altered DNA molecules may be expressed recombinantly in appropriate host cells to produce the modified protein.

The SOE method uses two amplified oligonucleotide products, which have complementary ends as primers and which include an altered codon at the locus at which the mutation is desired, to produce a hybrid product. A second amplification reaction that uses two primers that anneal at the non-overlapping ends amplify the hybrid to produce DNA that has the desired alteration.

In certain embodiments, the heterogeneity of preparations may be reduced by mutagenizing VEGF to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. VEGF is modified by deleting or replacing a site(s) that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of VEGF peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of VEGF or for retention of the ability to bind to a VEGF receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified VEGF is conjugated with a single species of cytotoxic conjugate.

Alternatively, the contribution of each cysteine to the ability to bind to VEGF may be determined empirically. Each cysteine residue may be systematically replaced with a conservative amino acid change (see Table 1, above) or deleted. The resulting mutein is tested for the requisite biological activity: the ability to bind to growth factor receptors and internalize. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. Each of the remaining cysteine residues may be systematically deleted and/or replaced by a serine residue or other residue that would not be expected to alter the structure of the protein. The resulting peptide is tested for biological activity. If the cysteine residue is necessary for

retention of biological activity it is not deleted; if it not necessary, then it is preferably replaced with a serine or other residue that should not alter the secondary structure of the resulting protein. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a vascular endothelial growth factor receptor and internalize may be determined. It is noted, however, that modified or mutant heparin-binding growth factors may exhibit reduced or no proliferative activity, but may be suitable for use herein, if they retain the ability to target a linked cytotoxic agent to cells bearing receptors to which the unmodified heparin-binding growth factor binds and result in internalization of the cytotoxic moiety. Monomeric forms of VEGF₁₂₁ contains 9 cysteines and each of VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆ contain 7 additional cysteine residues in the region not present in VEGF₁₂₁. Any of the 7 are likely to be non-essential for targeting and internalization of linked cytotoxic agents. Recently, the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys-145 in dimerization and biological activity was assessed (Claffery et al., *Biochem. Biophys. Acta* 1246:1-9, 1995). Dimerization requires Cys-25, Cys-56, and Cys-67. Substitution of any one of these cysteine residues resulted in secretion of a monomeric VEGF, which was inactive in both vascular permeability and endothelial cell mitotic assays. In contrast, substitution of Cys 145 had no effect on dimerization, although biological activities were somewhat reduced. Substitution of Cys-101 did not result in the production of a secreted or cytoplasmic protein. Thus, substitution of Cys-145 is preferred.

For chemical conjugates, the VEGF monomers are preferably linked via non-essential cysteine residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, preferably the VEGF is dimerized prior to linkage to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

It appears that all of the cysteines that are shared among the four VEGF monomers, VEGF₁₂₁, VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆ are required. Other cysteines that are present in VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆, that are not present in VEGF₁₂₁, may be modified, and the resulting modified monomer tested for ability to form dimers and for the requisite biological activities.

In particular, the VEGF molecules exemplified herein (SEQ ID NOs. 25-28) have cysteines at positions 52, 77, 83, 86, 87, 94, 128, and 130 in all VEGF monomers, and elsewhere in all monomers except for VEGF₁₂₁. It appears that the cysteines at residues 77, 86, 87, and 130 are required for intrachain binding and, thus,

should not be replaced. In order to decrease the potential for aggregate formation, when monomers, other than VEGF₁₂₁, are used it may be desirable to replace the cysteine residues at positions other than 52, 77, 83, 86, 87, 94, 128, and 130, particularly, those in the heparin binding domain in VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆ may be replaced with a conservative substitution, such as with a serine residue. Any replacements, however, should be checked for retention of the requisite binding and internalization properties. Each cysteine residue may be systematically replaced with a conservative amino acid change or deleted. The resulting mutein is tested for the requisite biological activity, the ability to bind to VEGF receptors and internalize linked targeted moieties. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a VEGF receptor and internalize may be determined.

The VEGF polypeptide may also be modified by addition of one or more cysteine residues at or near the C- or N-terminus, preferably the N-terminus, in order to render it more amenable to chemical conjugation by providing a readily available non-essential cysteine residue. VEGF has been modified herein by addition of Cys residues at or near the N-terminus in order to render them more amenable for chemical conjugation. Any VEGF may be modified for use herein by replacement of one or more cysteine residues that are not required for binding to a VEGF receptor and internalization of the targeted agent. These modified forms of VEGF are particularly suitable for chemical conjugation to linkers and/or targeted agents.

VEGF polypeptides may be isolated by methods known to those of skill in the art or may be prepared by expression of DNA encoding a VEGF protein (*see, e.g.,* Peretz et al. (1992) *Biochem. Biophys. Res. Commun.* 182:1340-1347; U.S. Patent No. 4,456,550 to Dvorak et al.; U.S. Patent No. 5,219,739 to Tischer et al.; U.S. Patent No. 5,194,596 to Tisher et al.; U.S. Patent No. 5,240,848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications serial nos. 07/351,361, 07/369,424, 07/389,722, to Genentech, Inc., and any U.S. Application Nos. 07/351,361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 A1 and EP 0 476 983 A1 to Merck & Co.; Houck et al. (1991) *Mol. Endo.* 5:1806-1814; see also SEQ ID Nos. 18-28 herein). It is understood herein that the key property of any VEGF polypeptide or fragment thereof is the ability, either as monomer or as a dimer, to bind to VEGF receptors and to be internalized by cells bearing such receptors.

B. Targeted agents**1. Cytotoxic agents**

Cytotoxic agent refers to a molecule capable of inhibiting cell function. Cytotoxic agents include any agent that, upon internalization, by a eukaryotic cell, inhibits growth or proliferation of the cell, either by killing the cell or inhibiting a metabolic pathway, transcription, or translation such that cell proliferation slows or stops. Any agent that, when internalized inhibits or destroys cell growth, cell proliferation or other essential cell functions is suitable for use herein. Cytotoxic agents include ribosome inactivating proteins, small metabolic inhibitors, antisense nucleic acids, toxic drugs, such as anticancer agents, and small molecules, such as light activated porphyrins. Ribosome inactivating proteins, such as saporin, are the preferred cytotoxic protein agents for use herein and nucleic acids are the preferred non-peptide agents.

Such cytotoxic agents, include, but are not limited to, saporin, the ricins, abrin and other RIPs, *Pseudomonas* exotoxin, inhibitors of DNA, RNA or protein synthesis, including antisense nucleic acids and other metabolic inhibitors that are known to those of skill in this art. Saporin is preferred, but other suitable RIPs include, but are not limited to, ricin, ricin A chain, maize RIP, gelonin, diphtheria toxin and diphtheria toxin A chain (see, e.g., U.S. Patent No. 4,675,382), trichosanthin, tritin, pokeweed antiviral protein (PAP), mirabilis antiviral protein (MAP), Dianthins 32 and 30, abrin, monordin, bryodin, bryodin2 (PCT application W0 95/11977), shiga, cytotoxically active fragments of cytotoxins and others known to those of skill in this art (see, e.g., Barbieri et al. (1982) *Cancer Surveys* 1:489-520 and European published patent application No. 466,222, incorporated herein by reference, which provide lists of numerous RIPs and their sources; see also, U.S. Patent No. 5,248,608).

The selected cytotoxic agent is, if necessary, derivatized to produce a group reactive with a cysteine on the selected VEGF. If derivatization results in a mixture of reactive species, a mono-derivatized form of the cytotoxic agent can be isolated and then conjugated to the selected VEGF.

30

a. Ribosome inactivating proteins

Ribosome-inactivating-proteins (RIPs), which include ricin, abrin and saporin, are plant proteins that catalytically inactivate eukaryotic ribosomes. RIPs inactivate ribosomes by interfering with the protein elongation step of protein synthesis. For example, the RIP saporin (hereinafter also referred to as SAP) has been shown to enzymatically inactivate the 60S ribosome by cleavage of the N-glycosidic bond of the adenine at position 4324 in the rat 28S ribosomal RNA (rRNA). Some RIPs, such as

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the toxins abrin and ricin, contain two constituent chains: a cell-binding chain that mediates binding to cell surface receptors and internalization of the molecule; and an enzymatically active chain responsible for protein synthesis inhibitory activity. Such RIPs are type II RIPs. Other RIPs, such as the saporins, are single chains and are designated type I RIPs. Because such RIPs lack a cell-binding chain, they are far less toxic to whole cells than the RIPs that have two chains.

Several structurally related saporins have been isolated from seeds and leaves of the plant *Saponaria officinalis* (soapwort). Among these, SAP-6 is the most active and abundant, representing 7% of total seed proteins. Saporin is very stable, has a high isoelectric point, does not contain carbohydrates, and is resistant to denaturing agents, such as sodium dodecyl sulfate (SDS), and a variety of proteases. The amino acid sequences of several saporin-6 isoforms from seeds are known and there appear to be families of saporin RIPs differing in a few amino acid residues. Because saporin is a type I RIP, it does not possess a cell-binding chain. Consequently, its toxicity to whole cells is much lower than the other toxins, such as ricin and abrin. When internalized by eukaryotic cells, however, its cytotoxicity is 100- to 1000-fold more potent than ricin A chain.

Saporin is preferred herein. SO-4 and SO-6 are preferred saporin molecules. SAP-6 (also called SO-6) is particularly preferred. The saporin polypeptides include any of the isoforms of saporin that may be isolated from *Saponaria officinalis* or related species or modified form that retain cytotoxic activity. Such modified forms have amino acid substitutions, deletions, insertions or additions but still express substantial ribosome-inactivating activity. Purified preparations of saporin are frequently observed to include several molecular isoforms of the protein. It is understood that differences in amino acid sequences can occur in saporin from different species as well as between saporin molecules from individual organisms of the same species. In particular, such modified saporin may be produced by modifying the DNA encoding the protein (*see, e.g.*, published International PCT Application WO 93/25688 (Serial No. PCT/US93/05702), United States Application Serial No. 07/901,718; *see, also*, U.S. Patent Application No. 07/885,242 filed May 20, 1992, and Patent No. 1231914, granted in Italy on January 15, 1992) by altering one or more amino acids or deleting or inserting one or more amino acids, such as a cysteine that may render it easier to conjugate to VEGF or other cell surface binding protein. Any such protein, or portion thereof, that, when conjugated to VEGF as described herein, exhibits cytotoxicity in standard *in vitro* or *in vivo* assays within at least about an order of magnitude of the saporin conjugates described herein is contemplated for use herein.

Thus, the SAP used herein includes any protein that is isolated from natural sources or that is produced by recombinant expression (*see, e.g.*, copending published International PCT Application WO 93/25688 (Serial No. PCT/US93/05702) and United States Application Serial No. 07/901,718, filed June 16, 1992).

5 Some of the DNA molecules provided herein encode saporin that has substantially the same amino acid sequence and ribosome-inactivating activity as that of saporin-6 (SO-6), including any of four isoforms, which have heterogeneity at amino acid positions 48 and 91 (*see, e.g.*, Maras et al., *Biochem. Internat.* 21:631-638, 1990, and Barra et al., *Biotechnol. Appl. Biochem.* 13:48-53, 1991; GB Patent 2,216,891 B and EP Patent 89306106). Other suitable saporin polypeptides include other members of the multi-gene family coding for isoforms of saporin-type ribosome-inactivating proteins including SO-1 and SO-3 (Fordham-Skelton et al., *Mol. Gen. Genet.* 221:134-138, 1990), SO-2 (*see, e.g.*, U.S. Application Serial No. 07/885,242, which corresponds to GB 2,216,891; *see, also*, Fordham-Skelton et al., *Mol. Gen. Genet.* 15 229:460-466, 1991), SO-4 (*see, e.g.*, GB 2,194,241 B; *see, also*, Lappi et al., *Biochem. Biophys. Res. Commun.* 129:934-942, 1985) and SO-5 (*see, e.g.*, GB 2,194,241 B; *see, also*, Montecucchi et al., *Int. J. Peptide Protein Res.* 33:263-267, 1989).

20 **b. Nucleic acids encoding other ribosome-inactivating proteins and cytocides**

In addition to saporin discussed above, other cytocides that inhibit protein synthesis are useful in the present invention. The gene sequences for these cytocides may be isolated by standard methods, such as PCR, probe hybridization of genomic or cDNA libraries, antibody screenings of expression libraries, or clones 25 obtained from commercial or other sources. The DNA sequences of many of these cytocides are well known, including ricin A chain (Genbank Accession No. X02388); maize ribosome-inactivating protein (Genbank Accession No. L26305); gelonin (Genbank Accession No. L12243; PCT Application WO 92/03155; U.S. Patent No. 5,376,546; diphtheria toxin (Genbank Accession No. K01722); trichosanthin (Genbank 30 Accession No. M34858); tritin (Genbank Accession No. D13795); pokeweed antiviral protein (Genbank Accession No. X78628); mirabilis antiviral protein (Genbank Accession No. D90347); dianthin 30 (Genbank Accession No. X59260); abrin (Genbank Accession No. X55667); shiga (Genbank Accession No. M19437); and *Pseudomonas* exotoxin (Genbank Accession Nos. K01397, M23348).

35 DNA encoding SAP or any cytotoxic agent may be used in the recombinant methods provided herein. In instances in which the cytotoxic agent does not contain a cysteine residue, such as instances in which DNA encoding SAP is

selected, the DNA may be modified to include a cysteine codon. The codon may be inserted into any locus that does not reduce or reduces by less than about one order of magnitude the cytotoxicity of the resulting protein may be selected. Such locus may be determined empirically by modifying the protein and testing it for cytotoxicity in an assay, such as a cell-free protein synthesis assay. The preferred loci in SAP for insertion of the cysteine residue is at or near the N-terminus (within about 20 residues, preferably 10 residues, of the N-terminus).

2. Expression of cytotoxic agents

Host organisms include those organisms in which recombinant production of heterologous proteins have been carried out and in which the cytotoxic agent, such as saporin is not toxic or of sufficiently low toxicity to permit expression before cell death. Presently preferred host organisms are strains of bacteria. Most preferred host organisms are strains of *E. coli*, particularly, BL21(DE3) cells (Novagen, Madison, WI).

The DNA encoding the cytotoxic agent, such as saporin protein, is introduced into a plasmid in operative linkage to an appropriate promoter for expression of polypeptides in a selected host organism. The presently preferred saporin proteins are saporin proteins that have been modified by addition of a Cys residue or replacement of a non-essential residue at or near the amino- or carboxyl terminus of the saporin with Cys. Saporin, such as that of SEQ ID No. 7 has been modified by insertion of Met-Cys residue at the N-terminus is preferred. It may additionally be modified by replacement of the Asn or Ile residue at positions 4 and 10, respectively, with cysteine (see Example 4). The DNA fragment encoding the saporin may also include a protein secretion signal that functions in the selected host to direct the mature polypeptide into the periplasm or culture medium. The resulting saporin protein can be purified by methods routinely used in the art, including, methods described hereinafter in the Examples.

Methods of transforming suitable host cells, preferably bacterial cells, and more preferably *E. coli* cells, as well as methods applicable for culturing said cells containing a gene encoding a heterologous protein, are generally known in the art. See, for example, Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.

The DNA construct encoding the saporin protein is introduced into the host cell by any suitable means, including, but not limited to transformation employing plasmids, bacterial phage vectors, transfection, electroporation, lipofection, and the like. The heterologous DNA can optionally include sequences, such as origins of

replication that allow for the extrachromosomal maintenance of the saporin-containing plasmid, or can be designed to integrate into the genome of the host (as an alternative means to ensure stable maintenance in the host).

Positive transformants can be characterized by Southern blot analysis
5 (Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY) for the site of DNA integration; Northern blots for inducible-promoter-responsive saporin gene expression; and product analysis for the presence of saporin-containing proteins in either the cytoplasm, periplasm, or the growth media.

10 Once the saporin-encoding DNA fragment has been introduced into the host cell, the desired saporin-containing protein is produced by subjecting the host cell to conditions under which the promoter is induced, whereby the operatively linked DNA is transcribed. In a preferred embodiment, such conditions are those that induce expression from the *E. coli* lac operon. The plasmid containing the DNA encoding the
15 saporin-containing protein also includes the lac operator region within the promoter and may also include the lac I gene encoding the lac repressor protein (lacI8) (*see, e.g.*, Muller-Hill et al. (1968) *Proc. Natl. Acad. Sci. USA* 59:1259-12649). The lac repressor represses the expression from the lac promoter until induced by the addition of IPTG in an amount sufficient to induce transcription of the DNA encoding the saporin-
20 containing protein.

The expression of saporin in *E. coli* is, thus accomplished in a two-stage process. In the first stage, a culture of transformed *E. coli* cells is grown under conditions in which the expression of the saporin-containing protein within the transforming plasmid, preferably encoding a saporin, such as described in Example 4, is
25 repressed by virtue of the lac repressor. In this stage cell density increases. When an optimum density is reached, the second stage commences by addition of IPTG, which prevents binding of repressor to the operator thereby inducing the lac promoter and transcription of the saporin-encoding DNA.

In a preferred embodiment, the promoter is the T7 RNA polymerase
30 promoter, which may be linked to the lac operator and the *E. coli* host strain includes DNA encoding T7 RNA polymerase operably linked to the lac operator and a promoter, preferably the lacUV5 promoter. A preferred plasmid is pET 11a (Novagen, Madison, WI), which contains the T7lac promoter, T7 terminator, the inducible *E. coli* lac operator, and the lac repressor gene. The plasmid pET 15b (Novagen, Madison, WI),
35 which contains a His-TagTM leader sequence (SEQ. ID No. 36) for use in purification with a His column and a thrombin cleavage site that permits cleavage following purification over the column, the T7-lac promoter region and the T7 terminator, has

been used herein for expression of saporin. Addition of IPTG induces expression of the T7 RNA polymerase and the T7 promoter, which is recognized by the T7 RNA polymerase.

Transformed strains, which are of the desired phenotype and genotype,
5 are grown in fermentors by suitable methods well known in the art. In the first, or growth stage, expression hosts are cultured in defined minimal medium lacking the inducing condition, preferably IPTG. When grown in such conditions, heterologous gene expression is completely repressed, which allows the generation of cell mass in the absence of heterologous protein expression. Subsequent to the period of growth
10 under repression of heterologous gene expression, the inducer, preferably IPTG, is added to the fermentation broth, thereby inducing expression of any DNA operatively linked to an IPTG-responsive promoter (a promoter region that contains lac operator). This last stage is the induction stage.

The resulting saporin-containing protein can be suitably isolated from
15 the other fermentation products by methods routinely used in the art, *e.g.*, using a suitable affinity column as described in the Examples; precipitation with ammonium sulfate; gel filtration; chromatography, preparative flat-bed iso-electric focusing; gel electrophoresis, high performance liquid chromatography (HPLC); and the like. A method for isolating saporin is provided in Example 1 (see, also Lappi et al. ((1985)
20 *Biochem. Biophys. Res. Commun.*, 129:934-942). The expressed saporin protein is isolated from either the cytoplasm, periplasm, or the cell culture medium (*see*, discussion below and Examples).

3. Porphyrins

25 Porphyrins are well known light activatable toxins that can be readily cross-linked to proteins (*see, e.g.*, U.S. Patent No. 5,257,970; U.S. Patent No. 5,252,720; U.S. Patent No. 5,238,940; U.S. Patent No. 5,192,788; U.S. Patent No. 5,171,749; U.S. Patent No. 5,149,708; U.S. Patent No. 5,202,317; U.S. Patent No. 5,217,966; U.S. Patent No. 5,053,423; U.S. Patent No. 5,109,016; U.S. Patent No.
30 5,087,636; U.S. Patent No. 5,028,594; U.S. Patent No. 5,093,349; U.S. Patent No. 4,968,715; U.S. Patent No. 4,920,143 and International Application WO 93/02192).

Porphyrins are conjugated to proteins by direct covalent bonds using, for example, a carbodiimide. Linkage may be effected by treatment of VEGF with 1-ethyl-3-(3-dimethylamino propyl) carbodiimide in the presence of a reaction medium
35 such as DMSO. For other methods see U.S. Patent No. 4,968,715. The porphyrin-VEGF conjugates may be administered topically or systemically. Activation of the

porphyrin is by irradiating light chosen to match the maximum absorbance of the porphyrin-type photosensitizer.

4. Nucleic acids for targeted delivery

5 The conjugates provided herein are also designed to deliver nucleic acids to targeted cells. The nucleic acids include those intended to deliver a cytotoxic signal to a cell or to modify expression of genes and thereby effect genetic therapy. Examples of nucleic acids include antisense RNA, DNA, ribozymes and oligonucleotides that bind proteins. The nucleic acids can also include RNA trafficking signals, such as viral
10 packaging sequences (*see, e.g.,* Sullenger et al. (1994) *Science* 262:1566-1569). The nucleic acids also include DNA molecules that encode intact genes or that encode proteins useful for gene therapy or for effecting cell cytotoxicity. Especially of interest are DNA molecules that encode an enzyme that results in cell death or renders a cell
15 susceptible to cell death upon the addition of another product. For example, saporin is an enzyme that cleaves rRNA and inhibits protein synthesis. Other enzymes that inhibit protein synthesis are especially well suited for the present invention. Other enzymes may be used where the enzyme activates a compound with little or no cytotoxicity into a toxic product.

DNA (or RNA) that may be delivered to a cell to effect genetic therapy
20 includes DNA that encodes tumor-specific cytotoxic molecules, such as tumor necrosis factor, viral antigens and other proteins to render a cell susceptible to anti-cancer agents, and DNA encoding genes, such as the defective gene (CFTR) associated with cystic fibrosis (*see, e.g.,* International Application WO 93/03709, which is based on U.S. Application Serial No. 07/745,900; and Riordan et al. (1989) *Science* 245:1066-
25 1073), to replace defective genes.

Nucleic acids and oligonucleotides for use as described herein can be synthesized by any method known to those of skill in this art (*see, e.g.,* WO 93/01286, which is based on U.S. Application Serial No. 07/723,454; U.S. Patent No. 5,218,088; U.S. Patent No. 5,175,269; U.S. Patent No. 5,109,124). Identification of
30 oligonucleotides and ribozymes for use as antisense agents as well selection of DNA encoding genes for targeted delivery for genetic therapy, as is well within the skill in this art. For example, the desirable properties, lengths and other characteristics of such oligonucleotides are well known. Antisense oligonucleotides are designed to resist degradation by endogenous nucleolytic enzymes and include, but are not limited to:
35 phosphorothioate, methylphosphonate, sulfone, sulfate, ketyl, phosphorodithioate, phosphoramidate, phosphate esters, and other such linkages (*see, e.g.,* Agrwal et al., *Tetrahedron Lett.* 28:3539-3542 (1987); Miller et al., *J. Am. Chem. Soc.* 93:6657-6665

(1971); Stec et al., *Tetrahedron Lett.* 26:2191-2194 (1985); Moody et al., *Nucl. Acids Res.* 12:4769-4782 (1989); Uznanski et al., *Nucl. Acids Res.* (1989); Letsinger et al., *Tetrahedron* 40:137-143 (1984); Eckstein, *Annu. Rev. Biochem.* 54:367-402 (1985); Eckstein, *Trends Biol. Sci.* 14:97-100 (1989); Stein In: *Oligodeoxynucleotides*.
5 *Antisense Inhibitors of Gene Expression*, Cohen, Ed, Macmillan Press, London, pp. 97-117 (1989); Jager et al., *Biochemistry* 27:7237-7246 (1988)).

a. Antisense nucleotides

Antisense nucleotides are oligonucleotides that bind in a sequence-specific manner to nucleic acids, such as mRNA or DNA. When bound to mRNA that
10 has complementary sequences, antisense prevents translation of the mRNA (*see, e.g.*, U.S. Patent No. 5,168,053 to Altman et al.; U.S. Patent No. 5,190,931 to Inouye, U.S. Patent No. 5,135,917 to Burch; U.S. Patent No. 5,087,617 to Smith and Clusel et al. (1993) *Nucl. Acids Res.* 21:3405-3411, which describes dumbbell antisense
15 oligonucleotides). Triplex molecules refer to single DNA strands that bind duplex DNA forming a colinear triplex molecule and thereby prevent transcription (*see, e.g.*, U.S. Patent No. 5,176,996 to Hogan et al., which describes methods for making synthetic oligonucleotides that bind to target sites on duplex DNA).

Particularly useful antisense nucleotides and triplex molecules are
20 molecules that are complementary or bind to the sense strand of DNA or mRNA that encodes an oncogene, such as bFGF, int-2, hst-1/K-FGF, FGF-5, hst-2/FGF-6, FGF-8. Other useful antisense oligonucleotides include those that are specific for IL-8 (*see, e.g.*, U.S. Patent No. 5,241,049; and International applications WO 89/004836; WO 90/06321; WO 89/10962; WO 90/00563; and WO 91/08483, and the corresponding
25 U.S. applications for descriptions of DNA encoding IL-8 and amino acid sequences of IL-8), which can be linked to bFGF for the treatment of psoriasis, anti-sense oligonucleotides that are specific for nonmuscle myosin heavy chain and/or c-myc (*see, e.g.*, Simons et al. (1992) *Circ. Res.* 70:835-843; WO 93/01286, which is based on U.S. application Serial No. 07/723,454; LeClerc et al. (1991) *J. Am. Coll. Cardiol.* 17
30 (2 Suppl. A):105A; Ebbecke et al. (1992) *Basic Res. Cardiol.* 87:585-591), which can be targeted by an FGF to inhibit smooth muscle cell proliferation, such as that following angioplasty and thereby prevent restenosis or inhibit viral gene expression in transformed or infected cells.

b. Ribozymes

35 A ribozyme is an RNA molecule that specifically cleaves RNA substrates, such as mRNA, and thus inhibit or interfere with cell growth or expression.

There are at least five classes of ribozymes that are known that are involved in the cleavage and/or ligation of RNA chains. Ribozymes can be targeted to any RNA transcript and can catalytically cleave such transcript (*see, e.g.*, U.S. Patent No. 5,272,262; U.S. Patent No. 5,144,019; and U.S. Patent Nos. 5,168,053, 5,180,818, 5,116,742 and 5,093,246 to Cech et al., which described ribozymes and methods for production thereof). Any such ribosome may be linked to the growth factor for delivery to VEGF-receptor bearing cells.

The ribozymes may be delivered to the targeted cells, such tumor cells that express a receptor to which VEGF binds and upon binding is internalized, as DNA encoding the ribozyme linked to a eukaryotic promoter, such as a eukaryotic viral promoter, generally a late promoter, such that upon introduction into the nucleus, the ribozyme will be directly transcribed. In such instances, the construct will also include a nuclear translocation sequence (NTS; *see* Table 2, below), generally as part of the growth factor or as part of a linker between the growth factor and linked DNA.

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c. Nucleic acids encoding therapeutic products

Among the DNA that encodes therapeutic products contemplated for use is DNA encoding correct copies of defective genes, such as the defective gene (CFTR) associated with cystic fibrosis (*see, e.g.*, International Application WO 93/03709, which is based on U.S. Application Serial No. 07/745,900; and Riordan et al. (1989) *Science* 245:1066-1073), and anticancer agents, such as tumor necrosis factors, and cytotoxic agents, such as saporin to VEGF-receptor bearing cells. The conjugate should include an NTS. If the conjugate is designed such that the VEGF and linked DNA is cleaved in the cytoplasm, then the NTS should be included in a portion of the linker that remains bound to the DNA, so that, upon internalization, the conjugate will be trafficked to the nucleus. The nuclear translocation sequence (NTS) may be a heterologous sequence or a may be derived from the selected growth factor.

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d. Other nucleic acids

Extracellular protein binding oligonucleotides refer to oligonucleotides that specifically bind to proteins. Small nucleotide molecules refer to nucleic acids that target a receptor site.

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e. Coupling of nucleic acids to proteins

To effect chemical conjugation herein, the VEGF protein is linked to the nucleic acid either directly or via one or more linkers. Methods for conjugating nucleic acids, at the 5' ends, 3' ends and elsewhere, to the amino and carboxyl termini and other

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sites in proteins are known to those of skill in the art (for a review see *e.g.*, Goodchild, (1993) In: *Perspectives in Bioconjugate Chemistry*, Mears, Ed., American Chemical Society, Washington, D.C. pp. 77-99). For example, proteins have been linked to nucleic acids using ultraviolet irradiation (Sperling et al. (1978) *Nucleic Acids Res.* 5:2755-2773; Fiser et al. (1975) *FEBS Lett.* 52:281-283), bifunctional chemicals (Bäumert et al. (1978) *Eur. J. Biochem.* 89:353-359; and Oste et al. (1979) *Mol. Gen. Genet.* 168:81-86) photochemical cross-linking (Vanin et al. (1981) *FEBS Lett.* 124:89-92; Rinke et al. (1980) *J.Mol.Biol.* 137:301-314; Millon et al. (1980); *Eur. J. Biochem.* 110:485-454).

10 In particular, the reagents (N-acetyl-N'-(p-glyoxylylbenzoyl) cystamine and 2-iminothiolane have been used to couple DNA to proteins, such as α 2macroglobulin (α 2M) via mixed disulfide formation (see, Cheng et al. (1983) *Nucleic Acids Res.* 11:659-669). N-acetyl-N'-(p-glyoxylylbenzoyl)cystamine reacts specifically with nonpaired guanine residues and, upon reduction, generates a free
15 sulfhydryl group. 2-Iminothiolane reacts with proteins to generate sulfhydryl groups that are then conjugated to the derivatized DNA by an intermolecular disulfide interchange reaction. Any linkage may be used provided that, upon internalization of the conjugate the targeted nucleic acid is active. Thus, it is expected that cleavage of the linkage may be necessary, although it is contemplated that for some reagents, such
20 as DNA encoding ribozymes linked to promoters or DNA encoding therapeutic agents for delivery to the nucleus, such cleavage may not be necessary.

Thiol linkages can be readily formed using heterbiofunctional reagents. Amines have also been attached to the terminal 5' phosphate of unprotected oligonucleotides or nucleic acids in aqueous solutions by reacting the nucleic acid with
25 a water-soluble carbodiimide, such as 1-ethyl-3'[3-dimethylaminopropyl]carbodiimide (EDC) or N-ethyl-N'(3-dimethylaminopropylcarbodiimidehydrochloride (EDCI), in imidazole buffer at pH 6 to produce the 5'phosphorimidazolide. Contacting the 5'phosphorimidazolide with amine-containing molecules, such as a VEGF, and ethylenediamine, results in stable phosphoramidates (*see, e.g.*, Chu et al. (1983) *Nucleic
30 Acids Res.* 11:6513-6529; and WO 88/05077). In particular, a solution of DNA is saturated with EDC, at pH 6 and incubated with agitation at 4°C overnight. The resulting solution is then buffered to pH 8.5 by adding, for example about 3 volutes of 100 mM citrate buffer, and adding about 5 μ g - about 20 μ g of a VEGF, and agitating the resulting mixture at 4°C for about 48 hours. The unreacted protein may be removed
35 from the mixture by column chromatography using, for example, Sephadex G75 (Pharmacia) using 0.1 M ammonium carbonate solution, pH 7.0 as an eluting buffer. The isolated conjugate may be lyophilized and stored until used.

U.S. Patent No. 5,237,016 provides methods for preparing nucleotides that are bromoacetylated at their 5' termini and reacting the resulting oligonucleotides with thiol groups. Oligonucleotides derivatized at their 5'-termini bromoacetyl groups can be prepared by reacting 5'-aminohexyl-phosphoramidate oligonucleotides with
5 bromoacetic acid-N-hydroxysuccinimide ester as described in U.S. Patent No. 5,237,016. U.S. Patent No. 5,237,016 also describes methods for preparing thiol-derivatized nucleotides, which can then be reacted with thiol groups on the selected growth factor. Briefly, thiol-derivatized nucleotides are prepared using a 5'-phosphorylated nucleotide in two steps: (1) reaction of the phosphate group with imidazole
10 in the presence of a diimide and displacement of the imidazole leaving group with cystamine in one reaction step; and reduction of the disulfide bond of the cystamine linker with dithiothreitol (see, also, Orgel et al. ((1986) *Nucl. Acids Res.* 14:651, which describes a similar procedure). The 5'-phosphorylated starting oligonucleotides can be prepared by methods known to those of skill in the art (see, e.g., Maniatis et al. (1982)
15 *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, New York, p. 122).

The antisense oligomer or nucleic acid, such as a methylphosphonate oligonucleotide (MP-oligomer), may be derivatized by reaction with SPDP or SMPB. The resulting MP-oligomer may be purified by HPLC and then coupled to VEGF,
20 which may be modified replacement of one or more non-essential cysteine residues, as described above. The MP-oligomer (about 0.1 μ M) is dissolved in about 40-50 μ l of 1:1 acetonitrile/water to which phosphate buffer (pH 7.5, final concentration 0.1 M) and a 1 mg MP-oligomer in about 1 ml phosphate buffered saline is added. The reaction is allowed to proceed for about 5-10 hours at room temperature and is then quenched with
25 about 15 μ L 0.1 iodoacetamide. The VEGF-oligonucleotide conjugates can be purified on heparin sepharose Hi-Trap columns (1 ml, Pharmacia) and eluted with a linear or step gradient. The conjugate should elute in 0.6 M NaCl.

f. Nucleic acids encoding cytotoxins

30 A cytotoxicity-encoding agent is a nucleic acid molecule (DNA or RNA) that, upon internalization by a cell, and subsequent transcription and/or translation into a cytotoxic agent, is cytotoxic to a cell or inhibits cell growth by inhibiting protein synthesis.

Cytotoxins include saporin, the ricins, abrin and other ribosome-inactivating proteins, *Pseudomonas* exotoxin, diphtheria toxin, angiogenin, tritin,
35 dianthins 32 and 30, momordin, pokeweed antiviral protein, mirabilis antiviral protein.

bryodin, angiogenin, and shiga exotoxin, as well as other cytocides that are known to those of skill in the art.

Especially of interest are DNA molecules that encode an enzyme that results in cell death or renders a cell susceptible to cell death upon the addition of another product. For example, saporin, a preferred cytocide, is an enzyme that cleaves rRNA and inhibits protein synthesis. Other enzymes that inhibit protein synthesis are especially well suited for use in the present invention. In addition, enzymes may be used where the enzyme activates a compound with little or no cytotoxicity into a toxic product that inhibits protein synthesis.

In addition to saporin discussed above, other cytocides that inhibit protein synthesis are useful in the present invention. The gene sequences for these cytocides may be isolated by standard methods, such as PCR, probe hybridization of genomic or cDNA libraries, antibody screenings of expression libraries, or obtain clones from commercial or other sources. The DNA sequences of many of these cytocides are well known, including ricin A chain (Genbank Accession No. X02388); maize ribosome-inactivating protein (Genbank Accession No. L26305); gelonin (Genbank Accession No. L12243; PCT Application WO 92/03155; U.S. Patent No. 5,376,546; diphtheria toxin (Genbank Accession No. K01722); trichosanthin (Genbank Accession No. M34858); tritin (Genbank Accession No. D13795); pokeweed antiviral protein (Genbank Accession No. X78628); mirabilis antiviral protein (Genbank Accession No. D90347); dianthin 30 (Genbank Accession No. X59260); abrin (Genbank Accession No. X55667); shiga (Genbank Accession No. M19437) and *Pseudomonas* exotoxin (Genbank Accession Nos. K01397, M23348).

In the case of cytocide molecules such as the ribosome-inactivating proteins, very few molecules may need be present for cell killing. Indeed, only a single molecule of diphtheria toxoid introduced into a cell was sufficient to kill the cell. In other cases, it may be that propagation or stable maintenance of the construct is necessary to attain sufficient numbers or concentrations of the gene product for effective gene therapy. Examples of replicating and stable eukaryotic plasmids are found in the scientific literature.

In general, constructs will also contain elements necessary for transcription and translation. If the cytocide-encoding agent is DNA, then it must contain a promoter. The choice of the promoter will depend upon the cell type to be transformed and the degree or type of control desired. Promoters can be constitutive or active in any cell type, tissue specific, cell specific, event specific or inducible. Cell-type specific promoters and event type specific promoters are preferred. Examples of constitutive or nonspecific promoters include the SV40 early promoter (U.S. Patent No.

5,118,627), the SV40 late promoter (U.S. Patent No. 5,118,627), CMV early gene promoter (U.S. Patent No. 5,168,062), and adenovirus promoter. In addition to viral promoters, cellular promoters are also amenable within the context of this invention. In particular, cellular promoters for the so-called housekeeping genes are useful. Viral
5 promoters are preferred, because generally they are stronger promoters than cellular promoters.

Tissue specific promoters are particularly useful when a particular tissue type is to be targeted for transformation. By using one of this class of promoters, an extra margin of specificity can be attained. For example, when the indication to be
10 treated is ophthalmological, either the alpha-crystalline promoter or gamma-crystalline promoter is preferred. When a tumor is the target of gene delivery, cellular promoters for specific tumor markers or promoters more active in tumor cells should be chosen. Thus, to transform prostate tumor cells the prostate-specific antigen promoter is especially useful. Similarly, the tyrosinase promoter or tyrosinase-related protein
15 promoter is a preferred promoter for melanoma treatment. For B lymphocytes, the immunoglobulin variable region gene promoter, for T lymphocytes, the TCR receptor variable region promoter, for helper T lymphocytes, the CD4 promoter, for liver, the albumin promoter, are but a few examples of tissue specific promoters. Many other examples of tissue specific promoters are readily available to one skilled in the art.

20 Inducible promoters may also be used. These promoters include the MMTV LTR (PCT WO 91/13160), which is inducible by dexamethasone, metallothionein, which is inducible by heavy metals, and promoters with cAMP response elements, which are inducible by cAMP. By using an inducible promoter, the nucleic acid may be delivered to a cell and will remain quiescent until the addition of
25 the inducer. This allows further control on the timing of production of the therapeutic gene.

Event-type specific promoters are active only upon the occurrence of an event, such as tumorigenicity or viral infection. The HIV LTR is a well known example of an event-specific promoter. The promoter is inactive unless the *tat* gene
30 product is present, which occurs upon viral infection.

Additionally, promoters that are coordinately regulated with a particular cellular gene may be used. For example, promoters of genes that are coordinately expressed when a particular VEGF receptor gene is expressed may be used. Then, the nucleic acid will be transcribed when the VEGF receptor, such as VEGFR1, is
35 expressed, and not when VEGFR2 is expressed. This type of promoter is especially useful when one knows the pattern of VEGF receptor expression in a particular tissue.

so that specific cells within that tissue may be killed upon transcription of a cytotoxic agent gene without affecting the surrounding tissues.

Alternatively, cytocide gene products may be noncytotoxic but activate a compound, which is endogenously produced or exogenously applied, from a nontoxic form to a toxic product that inhibits protein synthesis.

The construct must contain the sequence that binds to the nucleic acid binding domain, if the domain binds in a sequence specific manner. As described below, the target nucleotide sequence may be contained within the coding region of the cytocide, in which case, no additional sequence need be incorporated. It may be desirable to have multiple copies of target sequence. If the target sequence is coding sequence, the additional copies must be located in non-coding regions of the cytocide-encoding agent. The target sequences of the nucleic acid binding domains are typically generally known. The target sequence may be readily determined, in any case. Techniques are generally available for establishing the target sequence (*e.g.*, see PCT Application WO 92/05285 and U.S. Serial No. 586,769).

Specificity of delivery is achieved by coupling a nucleic acid binding domain to a receptor-binding internalized ligand, either by chemical conjugation or by constructing a fusion protein. Linkers as described above may be used. The receptor-binding internalized ligand part confers specificity of delivery in a cell-specific manner. The choice of the receptor-binding internalized ligand to use will depend upon the receptor expressed by the target cells. The receptor type of the target cell population may be determined by conventional techniques such as antibody staining, PCR of cDNA using receptor-specific primers, and biochemical or functional receptor binding assays. It is preferable that the receptor be cell type specific or have increased expression or activity (*i.e.*, higher rate of internalization) within the target cell population.

The nucleic acid binding domain can be of two types, non-specific in its ability to bind nucleic acid, or highly specific so that the amino acid residues bind only the desired nucleic acid sequence. Nonspecific binding proteins, polypeptides, or compounds are generally polycations or highly basic. Lys and Arg are the most basic of the 20 common amino acids; proteins enriched for these residues are candidates for nucleic acid binding domains. Examples of basic proteins include histones, protamines, and repeating units of lysine and arginine. Poly-L-lysine is a well-used nucleic acid binding domain (*see* U.S. Patent Nos. 5,166,320 and 5,354,844). Other polycations, such as spermine and spermidine, may also be used to bind nucleic acids. By way of example, the sequence-specific proteins including Sp-1, AP-1, myoD and the *rev* gene product from HIV may be used. Specific nucleic acid binding domains can be cloned

in tandem, individually, or multiply to a desired region of the receptor-binding internalized ligand of interest. Alternatively, the domains can be chemically conjugated to each other.

The corresponding response elements that bind sequence-specific domains are incorporated into the construct to be delivered. Complexing the cytotoxic-encoding agent to the receptor-binding internalized ligand/nucleic acid binding domain allows specific binding of response element to the nucleic acid binding domain. Even greater specificity of binding may be achieved by identifying and using the minimal amino acid sequence that binds to the cytotoxic-encoding agent of interest. For example, phage display methods can be used to identify amino acids residues of varying length that will bind to specific nucleic acid sequences with high affinity. (See U.S. Patent No. 5,223,409.) The peptide sequence can then be cloned into the receptor-binding internalized ligand as a single copy or multiple copies. Alternatively, the peptide may be chemically conjugated to the receptor-binding internalized ligand. Incubation of the cytotoxic-encoding agent with the conjugated proteins will result in a specific binding between the two.

These complexes may be used to deliver nucleic acids that encode saporin or other cytotoxic proteins into cells that have appropriate receptors that are expressed, over-expressed or more active in internalization upon binding. The cytotoxic gene is cloned downstream of a mammalian promoter such as SV40, CMV, TK or Adenovirus promoter. As described above, promoters of interest may be active in any cell type, active only in a tissue-specific manner, such as α -crystalline or tyrosinase, event specific or inducible, such as the MMTV LTR.

Receptor-binding internalized ligands are prepared as discussed by any suitable method, including recombinant DNA technology, isolation from a suitable source, purchase from a commercial source, or chemical synthesis. The selected linker or linkers is (are) linked to the receptor-binding internalized ligands by chemical reaction, generally relying on an available thiol or amine group on the receptor-binding internalized ligands. Heterobifunctional linkers are particularly suited for chemical conjugation. Alternatively, if the linker is a peptide linker, then the receptor-binding internalized ligands, linker and nucleic acid binding domain can be expressed recombinantly as a fusion protein.

VEGF may be isolated from a suitable source or may be produced using recombinant DNA methodology, discussed below. To effect chemical conjugation herein, the growth factor protein is conjugated generally via a reactive amine group or thiol group to the nucleic acid binding domain directly or through a linker to the nucleic acid binding domain. The growth factor protein is conjugated either via its N-terminus.

C-terminus, or elsewhere in the polypeptide. In preferred embodiments, the growth factor protein is conjugated via a reactive cysteine residue to the linker or to the nucleic acid binding domain. The growth factor can also be modified by addition of a cysteine residue, either by replacing a residue or by inserting the cysteine, at or near the amino or carboxyl terminus, within about 20, preferably 10 residues from either end, and preferably at or near the amino terminus.

In certain embodiments, the heterogeneity of preparations may be reduced by mutagenizing the growth factor protein to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. The growth factor protein is modified by deleting or replacing a site(s) on the growth factor that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of heparin-binding growth factor peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of the growth factor or for retention of the ability to bind to a growth factor receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified heparin-binding growth factor is conjugated with a single species of cytotoxic conjugate.

Alternatively, the contribution of each cysteine to the ability to bind to VEGF receptors may be determined empirically. Each cysteine residue may be systematically replaced with a conservative amino acid change (see Table 1, above) or deleted. The resulting mutein is tested for the requisite biological activity: the ability to bind to growth factor receptors and internalize linked nucleic acid binding domain and agents. If the mutein retains this activity, then the cysteine residue is not required. Additional cysteines are systematically deleted and replaced and the resulting muteins are tested for activity. Each of the remaining cysteine residues may be systematically deleted and/or replaced by a serine residue or other residue that would not be expected to alter the structure of the protein. The resulting peptide is tested for biological activity. If the cysteine residue is necessary for retention of biological activity it is not deleted; if it not necessary, then it is preferably replaced with a serine or other residue that should not alter the secondary structure of the resulting protein. In this manner the minimum number and identity of the cysteines needed to retain the ability to bind to a heparin-binding growth factor receptor and internalize may be determined. It is noted, however, that modified or mutant heparin-binding growth factors may exhibit reduced or no proliferative activity, but may be suitable for use herein, if they retain the ability

to target a linked cytotoxic agent to cells bearing receptors to which the unmodified heparin-binding growth factor binds and result in internalization of the cytotoxic moiety. In the case of monomeric VEGF, VEGF₁₂₁ contains 9 cysteines and each of VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆ contain 7 additional residues in the region not present in VEGF₁₂₁. Any of the 7 are likely to be non-essential for targeting and internalization of linked cytotoxic agents. Recently, the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys-145 in dimerization and biological activity was assessed (Claffery et al., *Biochem. Biophys. Acta* 1246:1-9, 1995). Dimerization requires Cys-25, Cys-56, and Cys-67. Substitution of any one of these cysteine residues resulted in secretion of a monomeric VEGF, which was inactive in both vascular permeability and endothelial cell mitotic assays. In contrast, substitution of Cys 145 had no effect on dimerization, although biological activities were somewhat reduced. Substitution of Cys-101 did not result in the production of a secreted or cytoplasmic protein. Thus, substitution of Cys-145 is preferred.

The VEGF monomers are preferably linked via non-essential cysteine residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, preferably the VEGF is dimerized prior to linkage to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

Methods for chemical conjugation of proteins are known to those of skill in the art. The preferred methods for chemical conjugation depend on the selected components, but preferably rely on disulfide bond formation. For example, if the targeted agent is SPDP-derivatized saporin, then it is advantageous to dimerize the VEGF moiety prior coupling or conjugating to the derivatized saporin. If VEGF is modified to include a cysteine residue at or near the N-, preferably, or C- terminus, then dimerization should follow coupling to the nucleic acid binding domain. To effect chemical conjugation herein, the VEGF polypeptide is linked via one or more selected linkers or directly to the nucleic acid binding domain.

A nucleic acid binding domain is prepared for chemical conjugation. For chemical conjugation, a nucleic acid binding domain may be derivatized with SPDP or other suitable chemicals. If the binding domain does not have a Cys residue available for reaction, one can be either inserted or substituted for another amino acid. If desired, mono-derivatized species may be isolated, essentially as described.

For chemical conjugation, the nucleic acid binding domain may be derivatized or modified such that it includes a cysteine residue for conjugation to the receptor-binding internalized ligand. Typically, derivatization proceeds by reaction with SPDP. This results in a heterogeneous population. For example, nucleic acid binding domain that is derivatized by SPDP to a level of 0.9 moles pyridine-disulfide per mole of nucleic acid binding domain includes a population of non-derivatized, mono-derivatized and di-derivatized SAP. nucleic acid binding domain proteins, which are overly derivatized with SPDP, may lose ability to bind nucleic acid because of reaction with sensitive lysines (Lambert et al., *Cancer Treat. Res.* 37:175-209, 1988).

5 The quantity of non-derivatized nucleic acid binding domain in the preparation of the non-purified material can be difficult to judge and this may lead to errors in being able to estimate the correct proportion of derivatized nucleic acid binding domain to add to the reaction mixture.

Because of the removal of a negative charge by the reaction of SPDP with lysine, the three species, however, have a charge difference. The methods herein rely on this charge difference for purification of mono-derivatized nucleic acid binding domain by Mono-S cation exchange chromatography. The use of purified mono-derivatized nucleic acid binding domain has distinct advantages over the non-purified material. The amount of receptor-binding internalized ligand that can react with nucleic acid binding domain is limited to one molecule with the mono-derivatized material, and it is seen in the results presented herein that a more homogeneous conjugate is produced. There may still be sources of heterogeneity with the mono-derivatized nucleic acid binding domain used here but is acceptable as long as binding to the cytocide-encoding agent is not impacted.

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Because more than one amino group on the nucleic acid binding domain may react with the succinimidyl moiety, it is possible that more than one amino group on the surface of the protein is reactive. This creates potential for heterogeneity in the mono-derivatized nucleic acid binding domain. As an alternative to derivatizing to introduce a sulfhydryl, the nucleic acid binding domain can be modified by the introduction of a cysteine residue. Preferred loci for introduction of a cysteine residue include the N-terminus region, preferably within about one to twenty residues from the N-terminus of the nucleic acid binding domain. Using either methodology (reacting mono-derivatized nucleic acid binding domain introducing a Cys residue into nucleic acid binding domain), the resulting preparations of chemical conjugates are monogenous; compositions containing the conjugates also appear to be free of aggregates. As a preferred alternative, heterogeneity can be avoided by producing a

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fusion protein of receptor-binding internalized ligand and nucleic acid binding domain, as described below.

Expression of DNA encoding a fusion of a receptor-binding internalized ligand polypeptide linked to the nucleic acid binding domain results in a more homogeneous preparation of cytotoxic conjugates. Aggregate formation can be reduced in preparations containing the fusion proteins by modifying the receptor-binding internalized ligand, such as by removal of nonessential cysteines, and/or the nucleic acid binding domain to prevent interactions between conjugates via free cysteines.

DNA encoding the polypeptides may be isolated, synthesized or obtained from commercial sources or prepared as described herein. Expression of recombinant polypeptides may be performed as described herein; and DNA encoding these polypeptides may be used as the starting materials for the methods herein.

As described above, DNA encoding VEGF are described above. DNA may be prepared synthetically based on the amino acid or DNA sequence or may be isolated using methods known to those of skill in the art, such as PCR, probe hybridization of libraries, and the like or obtained from commercial or other sources.

As described herein, such DNA may then be mutagenized using standard methodologies to delete or replace any cysteine residues that are responsible for aggregate formation. If necessary, the identity of cysteine residues that contribute to aggregate formation may be determined empirically, by deleting and/or replacing a cysteine residue and ascertaining whether the resulting growth factor with the deleted cysteine forms aggregates in solutions containing physiologically acceptable buffers and salts. Loci for insertion of cysteine residues may also be determined empirically. Generally, regions at or near (within 20, preferably 10 amino acids) the C- or, preferably, the N-terminus are preferred.

The DNA construct encoding the fusion protein can be inserted into a plasmid and expressed in a selected host, as described above, to produce a recombinant receptor-binding internalized ligand—nucleic acid binding domain conjugate. Multiple copies of the chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will then be a multimer. Typically, two to six copies of the chimera are inserted, preferably in a head to tail fashion, into one plasmid.

To produce monogenous preparations of fusion protein, DNA VEGF is modified so that, upon expression, the resulting VEGF portion of the fusion protein does not include any cysteines available for reaction. In preferred embodiments, DNA encoding an VEGF polypeptide is linked to DNA encoding a nucleic acid binding domain. The DNA encoding the VEGF polypeptide or other receptor-binding

internalized ligand is modified in order to remove the translation stop codon and other transcriptional or translational stop signals that may be present and to remove or replace DNA encoding the available cysteines. The DNA is then ligated to the DNA encoding the nucleic acid binding domain polypeptide directly or via a linker region of one or more codons between the first codon of the nucleic acid binding domain and the last codon of the VEGF. The size of the linker region may be any length as long as the resulting conjugate binds and is internalized by a target cell. Presently, spacer regions of from about one to about seventy-five to ninety codons are preferred. The order of the receptor-binding internalized ligand and nucleic acid binding domain in the fusion protein may be reversed. If the nucleic acid binding domain is N-terminal, then it is modified to remove the stop codon and any stop signals.

If the VEGF or other ligand has been modified so as to lack mitogenic activity or other biological activities, binding and internalization may still be readily assayed by any one of the following tests or other equivalent tests. Generally, these tests involve labeling the ligand, incubating it with target cells, and visualizing or measuring intracellular label. For example, briefly, VEGF may be fluorescently labeled with FITC or radiolabeled with ^{125}I . Fluorescein-conjugated VEGF is incubated with cells and examined microscopically by fluorescence microscopy or confocal microscopy for internalization. When VEGF is labeled with ^{125}I , the labeled VEGF is incubated with cells at 4°C . Cells are temperature shifted to 37°C and washed with 2 M NaCl at low pH to remove any cell-bound VEGF. Label is then counted and thereby measuring internalization of VEGF. Alternatively, the ligand can be conjugated with an nucleic acid binding domain by any of the methods described herein and complexed with a plasmid encoding saporin. As discussed below, the complex may be used to transfect cells and cytotoxicity measured.

The DNA encoding the resulting receptor-binding internalized ligand—nucleic acid binding domain can be inserted into a plasmid and expressed in a selected host, as described above, to produce a monogenous preparation.

Multiple copies of the modified receptor-binding internalized ligand/nucleic acid binding domain chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will be a multimer. Typically two to six copies of the chimera are inserted, preferably in a head to tail fashion, into one plasmid. Merely by way of example, DNA encoding human bFGF- has been mutagenized using splicing by overlap extension (SOE). Each application of the SOE method uses two amplified oligonucleotide products, which have complementary ends as primers and which include an altered codon at the locus at which the mutation is desired, to produce a hybrid product. A second amplification

reaction that uses two primers that anneal at the non-overlapping ends amplify the hybrid to produce DNA that has the desired alteration.

The receptor-binding internalized ligand/nucleic acid binding domain is incubated with the cytocide-encoding agent, typically a DNA molecule, to be delivered under conditions that allow binding of the nucleic acid binding domain to the agent. Conditions will vary somewhat depending on the nature of the nucleic acid binding domain, but will typically occur in 0.1M NaCl and 20 mM HEPES or other similar buffer.

The desired application is the delivery of cytotoxic agents, such as saporin, in a non-toxic form. By delivering a nucleic acid molecule capable of expressing saporin, the timing of cytotoxicity may be exquisitely controlled. For example, if saporin is expressed under the control of a tissue-specific promoter, then uptake of the complex by cells having the tissue-specific factors necessary for promoter activation will result in the killing of those cells. On the other hand, if cells taking up the complex do not have those tissue-specific factors, the cells will be spared.

Merely by way of example, test constructs have been made and tested. One construct is a chemical conjugate of bFGF and poly-L-lysine. The bFGF molecule is a variant in which the Cys residue at position 96 has been changed to a serine; thus, only the Cys at position 78 is available for conjugation. This bFGF is called VEGF2-3. The poly-L-lysine was derivatized with SPDP and coupled to FGF2-3. This FGF2-3/poly-L-lysine conjugate was used to deliver a plasmid able to express the β -galactosidase gene.

The ability of a construct to bind nucleic acid molecules may be conveniently assessed by agarose gel electrophoresis. Briefly, a plasmid, such as pSV β , is digested with restriction enzymes to yield a variety of fragment sizes. For ease of detection, the fragments may be labeled with ^{32}P either by filling in of the ends with DNA polymerase I or by phosphorylation of the 5'-end with polynucleotide kinase following dephosphorylation by alkaline phosphatase. The plasmid fragments are then incubated with the receptor-binding internalized ligand/nucleic acid binding domain in this case, FGF2-3/poly-L-lysine in a buffered saline solution, such as 20 mM HEPES, pH 7.3, 0.1M NaCl. The reaction mixture is electrophoresed on an agarose gel alongside similarly digested, but nonreacted fragments. If a radioactive label was incorporated, the gel may be dried and autoradiographed. If no radioactive label is present, the gel may be stained with ethidium bromide and the DNA visualized through appropriate red filters after excitation with UV. Binding has occurred if the mobility of the fragments is retarded compared to the control. In the example case, the mobility of the fragments was retarded after binding with the FGF2-3/poly-L-lysine conjugate.

Further testing of the conjugate is performed to show that it binds to the cell surface receptor and is internalized into the cell. It is not necessary that the receptor-binding internalized ligand part of the conjugate retain complete biological activity. For example, VEGF is mitogenic on certain cell types. As discussed above, this activity may not always be desirable. If this activity is present, a proliferation assay is performed. Likewise, for each desirable activity, an appropriate assay may be performed. However, for application of the subject invention, the only criteria that need be met are receptor binding and internalization.

Receptor binding and internalization may be measured by the following three assays. (1) A competitive inhibition assay of the complex to cells expressing the appropriate receptor demonstrates receptor binding. (2) Receptor binding and internalization may be assayed by measuring β -gal expression (e.g., enzymatic activity) in cells that have been transformed with a complex of a β -gal containing plasmid condensed with a receptor-binding internalized ligand/nucleic acid binding domain. This assay is particularly useful for optimizing conditions to give maximal transformation. Thus, the optimum ratio of receptor-binding internalized ligand/nucleic acid binding domain to nucleic acid and the amount of DNA per cell may readily be determined by assaying and comparing the enzymatic activity of β -gal. As such, these first two assays are useful for preliminary analysis and failure to show receptor binding or β -gal activity does not per se eliminate a candidate receptor-binding internalized ligand/nucleic acid binding domain conjugate or fusion protein from further analysis. (3) The preferred assay is a cytotoxicity assay performed on cells transformed with a cytocide-encoding agent bound by receptor-binding internalized ligand/nucleic acid binding domain. While, in general, any cytotoxic molecule may be used, ribosome-inactivating proteins are preferred and saporin, or another type I ribosome-inactivating protein, is particularly preferred. A statistically significant reduction in cell number demonstrates the ability of the receptor-binding internalized ligand/nucleic acid binding domain conjugate or fusion to deliver nucleic acids into a cell.

30 C. Other elements

1. Nuclear translocation signals

As used herein, a nuclear translocation or targeting sequence (NTS) is a sequence of amino acids in a protein that are required for translocation of the protein into a cell nucleus. Examples of NTS are set forth in Table 2. below. Comparison with known NTSs, and if necessary testing of candidate sequences, should permit those of skill in the art to readily identify other amino acid sequences that function as NTSs.

As used herein, heterologous NTS refers to an NTS that is different from the NTS that occurs in the wild-type peptide, polypeptide, or protein. For example, the NTS may be derived from another polypeptide, it may be synthesized, or it may be derived from another region in the same polypeptide. A typical consensus NTS
5 sequence contains an amino-terminal proline or glycine followed by at least three basic residues in a array of seven to nine amino acids (*see, e.g.* Dang et al. (1989) *J. Biol. Chem.* 264:18019-18023, Dang et al. (1988) *Mol. Cell. Biol.* 8:4049-4058 and Table 2, which sets forth examples of NTSs and regions of proteins that share homology with known NTSs),

TABLE 2

SOURCE	SEQUENCE	SEQ ID NO.
SV40 large T	Pro ¹²⁶ LysLysArgLysValGlu	90
Polyoma large T	Pro ²⁷⁹ ProLysLysAlaArgGluVal	91
Human c-Myc	Pro ¹²⁰ AlaAlaLysArgValLysLeuAsp	92
Adenovirus E1A	Lys ²⁸¹ ArgProArgPro	93
Yeast mat α 2	Lys ³ IleProlleLys	94
c-Erb-A	A. Gly ²² LysArgLysArgLysSer	95
	B. Ser ¹²⁷ LysArgValAlaLysArgLysleu	96
	C. Ser ¹⁸¹ HisTrpLysGlnLysArgLysPhe	97
c-Myb	Pro ⁵²¹ LeuLeuLysLysIleLysGln	98
p53	Pro ³¹⁶ GlnProLysLysLysPro	99
Nucleolin	Pro ²⁷⁷ GlyLysArgLysLysGluMetThrLysGlnLysGluValPro	100
HIV Tat	Gly ⁴⁸ ArgLysLysArgArgGlnArgArgArgAlaPro	101
FGF-1	AsnTyrLysLysProLysLeu	102
FGF-2	HisPheLysAspProLysArg	103
FGF-3	AlaProArgArgArgLysLeu	72
FGF-4	IleLysArgLeuArgArg	75
FGF-5	GlyArgArg	-
FGF-6	IleLysArgGlnArgArg	76
FGF-7	IleArgValArgArg	84
VEGF ₁₈₉	LysArgLysArgLysLys (in EXON VI)	85
VEGF ₂₀₆	LysArgLysArgLysLys (in EXON VI)	85
PDGF	ProLysGlyLysHisArgLysPheLysHisThr	

* Superscript indicates position in protein

2. Cytoplasm-translocation signal

- 5 Cytoplasm-translocation signal sequence is a sequence of amino acids in a protein that cause retention of proteins in the lumen of the endoplasmic reticulum and/or translocate proteins to the cytosol. The signal sequence in mammalian cells is KDEL (Lys-Asp-Glu-Leu) (Munro and Pelham, *Cell* 48:899-907, 1987). Some modifications of this sequence have been made without loss of activity. For example,
- 10 the sequences RDEL (Arg-Asp-Glu-Leu) and KEEL (Lys-Glu-Glu-Leu) confer efficient or partial retention, respectively, in plants (Denecke et al., *Embo. J.* 11:2345-2355, 1992).

A cytoplasm-translocation signal sequence may be included in saporin or, for conjugates of VEGF with a nucleic acid binding domain, the sequence may reside in either part or both. If cleavable linkers are used in the conjugate, the cytoplasm-translocation signal is preferably included in saporin or the nucleic acid binding domain. Additionally, a cytoplasmic-translocation signal sequence may be included in VEGF, as long as it is placed so as not to interfere with receptor binding.

In addition, or alternatively, membrane-disruptive peptides may be incorporated into complexes of VEGF-nucleic acid binding domain and cytocide-encoding agent. Adenoviruses are known to enhance disruption of endosomes. Virus-free viral proteins, such as influenza virus hemagglutinin HA-2, may be useful in the present invention. Other proteins may be tested in the assays described herein to find specific endosome disrupting agents that enhance gene delivery. In general, these proteins and peptides are amphipathic (*see*, Wagner et al., *Adv. Drug. Del. Rev.* 14:113-135, 1994).

3. Linkers

A linker is a peptide or other molecule that couples a VEGF polypeptide to the targeted agent. The linker may be bound via the N- or C-terminus or an internal residue, but, typically within about 20 amino acids of either terminus of a VEGF and/or targeted agent. The linkers provided herein increase intracellular availability, serum stability, specificity and solubility of the conjugate or provide increased flexibility or relieve steric hindrance in the conjugate. For example, specificity or intracellular availability of the targeted agent of may be conferred by including a linker that is a substrate for certain proteases, such as a protease that is present in only certain subcellular compartments or that are present at higher levels in tumor cells than normal cells.

In order to increase the serum stability, solubility and/or intracellular concentration and to reduce steric hindrance caused by close proximity of VEGF and the targeted agent, one or more linkers is (are) inserted between the VEGF protein and the targeted moiety. These linkers include peptide linkers, such as intracellular protease substrates and peptides that increase flexibility or solubility of the linked moieties, and chemical linkers, such as acid labile linkers, ribozyme substrate linkers and others. Peptide linkers may be inserted using heterobiofunctional reagents, described below, or, preferably, are linked to VEGF by linking DNA encoding the substrate to the DNA encoding the VEGF protein and expressing the resulting chimera. In instances in which the targeted agent is a protein, such as a RIP, the DNA encoding the linker can be inserted between the DNA encoding the VEGF protein and the DNA encoding the targeted protein agent.

Chemical linkers may be inserted by covalently coupling the linker to the VEGF protein and the targeted agent. The heterobifunctional agents, described below, may be used to effect such covalent coupling.

5 **a. Protease substrates**

Peptides encoding protease-specific substrates are introduced between the VEGF protein and the targeted moiety. The peptides may be inserted using heterobiofunctional reagents, described below, or, preferably, are linked to VEGF by linking DNA encoding the substrate to the DNA encoding the VEGF protein and
10 expressing the resulting chimera. In instances in which the targeted agent is a protein, such as a RIP, the DNA encoding the linker can be inserted between the DNA encoding the VEGF protein and the DNA encoding the targeted protein agent. For example, DNA encoding substrates specific for intracellular proteases has been inserted between the DNA encoding the VEGF protein and a targeted agent, such as saporin.

15 Any protease specific substrate (*see, e.g.,* O'Hare et al. (1990) *FEBS* 273:200-204; Forsberg et al. (1991) *J. Protein Chem.* 10:517-526; Westby et al. (1992) *Bioconjugate Chem.* 3:375-381) may be introduced as a linker between the VEGF polypeptide and linked targeting agent as long as the substrate is cleaved in an intracellular compartment. Preferred substrates include those that are specific for
20 proteases that are expressed at higher levels in tumor cells or that are preferentially expressed in the endosome. The following substrates are among those contemplated for use in accord with the methods herein: cathepsin B substrate, cathepsin D substrate, trypsin substrate, thrombin substrate, and recombinant subtilisin substrate (XaaAspGluLeu SEQ ID NO. 50, particularly, PheAlaHisTyr, SEQ ID NO. 49).

25

b. Flexible linkers and linkers that increase the solubility of the conjugates

Flexible linkers and linkers that increase solubility of the conjugates are contemplated for use, either alone or with other linkers, such as the protease specific
30 substrate linkers. Such linkers include, but are not limited to, (Gly₄Ser)_n, (Ser₄Gly)_n and (AlaAlaProAla)_n (*see*, SEQ ID NO. 48) in which n is 1 to 6, preferably 1-4, such as:

- (1) Gly₄Ser SEQ ID NO. 40
CCATGGGCGG CGGCGGCTCT GCCATGG
35 (2) (Gly₄Ser)₂ SEQ ID NO. 41
CCATGGGCGG CGGCGGCTCT GCGGCGGCG GCTCTGCCAT GG
 (3) (Ser₄Gly)₄ SEQ ID NO. 42

CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCTC GTCGTCGTCG
GGCTCGTCGT CGTCGGGCGC CATGG

(4) (Ser₄Gly)₂ SEQ ID NO. 43

CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCGC CATGG

5 (5) (AlaAlaProAla)_n, where n is 1 to 4,
preferably 2 (see, SEQ ID NO.:48)

The linker Gly₄Ser (SEQ ID No. 40) is preferred for VEGF-VEGF conjugates. The linker Ala-Met is preferred for SAP-VEGF chemical conjugates, and
10 no linker is preferred for SAP-VEGF fusion proteins. In general, a linker length of 1 is preferred for conferring stability on the conjugates.

c. Heterobifunctional cross-linking reagents

Numerous heterobifunctional cross-linking reagents that are used to
15 form covalent bonds between amino groups and thiol groups and to introduce thiol groups into proteins, are known to those of skill in this art (see, e.g., the Pierce Catalog, ImmunoTechnology Catalog & Handbook, 1992-1993, which describes the preparation of and use of such reagents and provides a commercial source for such reagents; see, also, e.g., Cumber et al. (1992) *Bioconjugate Chem.* 3:397-401; Thorpe et al. (1987) *Cancer Res.* 47:5924-5931; Gordon et al. (1987) *Proc. Natl. Acad. Sci.* 84:308-312; Walden et al. (1986) *J. Mol. Cell Immunol.* 2:191-197; Carlsson et al. (1978) *Biochem. J.* 173: 723-737; Mahan et al. (1987) *Anal. Biochem.* 162:163-170; Wawryznaczk et al. (1992) *Br. J. Cancer* 66:361-366; Fattom et al. (1992) *Infection & Immun.* 60:584-589). These reagents may be used to form covalent bonds between the VEGF
25 polypeptide(s) with protease substrate peptide linkers and targeted protein agent. These reagents include, but are not limited to: N-succinimidyl-3-(2-pyridyldithio)propionate (SPDP; disulfide linker); sulfosuccinimidyl 6-[3-(2-pyridyldithio)propionamido]hexanoate (sulfo-LC-SPDP); succinimidyl oxycarbonyl- α -methyl benzyl thiosulfate (SMBT, hindered disulfate linker); succinimidyl 6-[3-(2-pyridyldithio)propionamido]hexanoate (LC-SPDP); sulfosuccinimidyl 4-(N-maleimidomethyl)cyclohexane-1-carboxylate (sulfo-SMCC); succinimidyl 3-(2-pyridyldithio)butyrate (SPDB; hindered disulfide bond linker); sulfosuccinimidyl 2-(7-azido-4-methylcoumarin-3-acetamide) ethyl-1,3'-dithiopropionate (SAED); sulfo-succinimidyl 7-azido-4-methylcoumarin-3-acetate (SAMCA); sulfosuccinimidyl 6-[α -methyl- α -(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-SMPT); 1,4-di-
35 [3'-(2'-pyridyldithio)propionamido]butane (DPDPB); 4-succinimidyl oxycarbonyl- α -methyl- α -(2-pyridylthio)toluene (SMPT, hindered disulfate linker); sulfosuccinimidyl 6-

α -methyl- α -(2-pyridyldithio)toluamido]hexanoate (sulfo-LC-SMPT); *m*-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS); *m*-maleimidobenzoyl-N-hydroxysulfosuccinimide ester (sulfo-MBS); N-succinimidyl(4-iodoacetyl)aminobenzoate (SIAB; thioether linker); sulfosuccinimidyl(4-iodoacetyl)amino benzoate (sulfo-SIAB); succinimidyl4(*p*-maleimidophenyl)butyrate (SMPB); sulfosuccinimidyl4-(*p*-maleimidophenyl)butyrate (sulfo-SMPB); azidobenzoyl hydrazide (ABH). These linkers should be particularly useful when used in combination with peptide linkers, such as those that increase flexibility.

10 **d. Acid cleavable, photocleavable and heat sensitive linkers**

Acid cleavable linkers include, but are not limited to, bismaleimideoxy propane; and adipic acid dihydrazide linkers (*see, e.g.*, Fattom et al. (1992) *Infection & Immun.* 60:584-589) and acid labile transferrin conjugates that contain a sufficient portion of transferrin to permit entry into the intracellular transferrin cycling pathway (*see, e.g.*, Welhöner et al. (1991) *J. Biol. Chem.* 266:4309-4314). Conjugates linked via acid cleavable linkers should be preferentially cleaved in acidic intracellular compartments, such as the endosome.

Photocleavable linkers are linkers that are cleaved upon exposure to light (*see, e.g.*, Goldmacher et al. (1992) *Bioconj. Chem.* 3:104-107, which linkers are herein incorporated by reference), thereby releasing the targeted agent upon exposure to light. Photocleavable linkers are linkers that are cleaved upon exposure to light are known (*see, e.g.*, Hazum et al. (1981) in *Pept., Proc. Eur. Pept. Symp., 16th*, Brunfeldt, K (Ed), pp. 105-110, which describes the use of a nitrobenzyl group as a photocleavable protective group for cysteine; Yen et al. (1989) *Makromol. Chem.* 190:69-82, which describes water soluble photocleavable copolymers, including hydroxypropylmethacrylamide copolymer, glycine copolymer, fluorescein copolymer and methylrhodamine copolymer; Goldmacher et al. (1992) *Bioconj. Chem.* 3:104-107, which describes a cross-linker and reagent therefor that undergoes photolytic degradation upon exposure to near UV light (350 nm); and Senter et al. (1985) *Photochem. Photobiol* 42:231-237, which describes nitrobenzyloxycarbonyl chloride cross linking reagents that produce photocleavable linkages), thereby releasing the targeted agent upon exposure to light. Such linkers would have particular use in treating dermatological or ophthalmic conditions that can be exposed to light using fiber optics. After administration of the conjugate, the eye or skin or other body part can be exposed to light, resulting in release of the targeted moiety from the conjugate. If the toxic moiety is a light activated porphyrin, light-exposure will also activate the porphyrin, thereby causing cell death. Use of photocleavable linkers should permit

administration of higher dosages of such conjugates compared to conjugates that release a cytotoxic agent upon internalization. Heat sensitive linkers would also have similar applicability.

5 **D. Expression vectors and host cells for expression of VEGF or targeted agents.**

DNA encoding the desired VEGF, polypeptide targeted agent or VEGF conjugate is inserted into a suitable vector and expressed in a suitable prokaryotic or eukaryotic host. Numerous suitable hosts and vectors are known and available to those
10 of skill in this art and may be purchased commercially or constructed according to published protocols using well known and available starting materials. Suitable eukaryotic host cells include insect cells, yeast cells, and animal cells. Suitable prokaryotic host cells include *E. coli*, strains of *Bacillus* and *Streptomyces*. *E. coli* is a preferred host cell.

15 The DNA construct is introduced into a plasmid for expression in a desired host. In preferred embodiments, the host is a bacterial host. The sequences of nucleotides in the plasmids that are regulatory regions, such as promoters and operators, are operationally associated with one another for transcription. The sequence of nucleotides encoding the growth factor or growth factor-chimera may also include
20 DNA encoding a secretion signal, whereby the resulting peptide is a precursor protein. The resulting processed protein may be recovered from the periplasmic space or the fermentation medium.

In preferred embodiments the DNA plasmids also include a transcription terminator sequence. The promoter regions and transcription terminators are each
25 independently selected from the same or different genes.

The plasmids used herein include a promoter in operable association with the DNA encoding the protein or polypeptide of interest and are designed for expression of proteins in a bacterial host. It has been found that tightly regulated promoters are preferred for expression of saporin. Suitable promoters for expression of
30 proteins and polypeptides herein are widely available and are well known in the art. Inducible promoters or constitutive promoters that are linked to regulatory regions are preferred. Examples of suitable inducible promoters and promoter regions include, but are not limited to: the *E. coli* lac operator responsive to isopropyl β -D-thiogalactopyranoside (IPTG; see, et al. Nakamura et al. (1979) *Cell* 18:1109-
35 1117); the metallothionein promoter metal-regulatory-elements responsive to heavy-metal (e.g., zinc) induction (see, e.g., U.S. Patent No. 4,870,009 to Evans et al.); the

phage T7lac promoter responsive to IPTG (*see, e.g.*, U.S. Patent No. 4,952,496; and Studier et al. (1990) *Meth. Enzymol.* 185:60-89) and the tac promoter. Other promoters include, but are not limited to, the T7 phage promoter and other T7-like phage promoters, such as the T3, T5 and SP6 promoters, the trp, lpp, and lac promoters, such as the lacUV5, from *E. coli*; the P10 or polyhedron gene promoter of baculovirus/insect cell expression systems (*see, e.g.*, U.S. Patent Nos. 5,243,041, 5,242,687, 5,266,317, 4,745,051, and 5,169,784) and inducible promoters from other eukaryotic expression systems.

Preferred promoter regions are those that are inducible and functional in *E. coli*. Examples of suitable inducible promoters and promoter regions include, but are not limited to: the *E. coli* lac operator responsive to isopropyl β -D-thiogalactopyranoside (IPTG; *see, et al.* Nakamura et al., *Cell* 18:1109-1117, 1979); the metallothionein promoter metal-regulatory-elements responsive to heavy-metal (*e.g.*, zinc) induction (*see, e.g.*, U.S. Patent No. 4,870,009 to Evans et al.); the phage T7lac promoter responsive to IPTG (*see, e.g.*, U.S. Patent No. 4,952,496; and Studier et al., *Meth. Enzymol.* 185:60-89, 1990) and the tac promoter.

The plasmids also preferably include a selectable marker gene or genes that are functional in the host. A selectable marker gene includes any gene that confers a phenotype on bacteria that allows transformed bacterial cells to be identified and selectively grown from among a vast majority of untransformed cells. Suitable selectable marker genes for bacterial hosts, for example, include the ampicillin resistance gene (Amp^r), tetracycline resistance gene (Tc^r) and the kanamycin resistance gene (Kan^r). The kanamycin resistance gene is presently preferred.

The plasmids may also include DNA encoding a signal for secretion of the operably linked protein. Secretion signals suitable for use are widely available and are well known in the art. Prokaryotic and eukaryotic secretion signals functional in *E. coli* may be employed. The presently preferred secretion signals include, but are not limited to, those encoded by the following *E. coli* genes: ompA, ompT, ompF, ompC, beta-lactamase, and alkaline phosphatase, and the like (von Heijne, *J. Mol. Biol.* 184:99-105, 1985). In addition, the bacterial pelB gene secretion signal (Lei et al., *J. Bacteriol.* 169:4379, 1987), the phoA secretion signal, and the cek2 functional in insect cell may be employed. The most preferred secretion signal is the *E. coli* ompA secretion signal. Other prokaryotic and eukaryotic secretion signals known to those of skill in the art may also be employed (*see, e.g.*, von Heijne, *J. Mol. Biol.* 184:99-105, 1985). Using the methods described herein, one of skill in the art can substitute secretion signals that are functional in either yeast, insect or mammalian cells to secrete proteins from those cells.

Preferred plasmids for transformation of *E. coli* cells include the pET expression vectors (*see*, U.S. patent 4,952,496; available from Novagen, Madison, WI; *see, also*, literature published by Novagen describing the system). Such plasmids include pET 11a, which contains the T7lac promoter, T7 terminator, the inducible
5 *E. coli* lac operator, and the lac repressor gene; pET 12a-c, which contains the T7 promoter, T7 terminator, and the *E. coli* ompT secretion signal; and pET 15b (Novagen, Madison, WI), which contains a His-TagTM leader sequence (Seq. ID No. 36) for use in purification with a His column and a thrombin cleavage site that permits cleavage following purification over the column; the T7-lac promoter region and the T7
10 terminator.

Other preferred plasmids include the pKK plasmids, particularly pKK 223-3, which contains the tac promoter, (available from Pharmacia; *see, also*, Brosius et al., *Proc. Natl. Acad. Sci.* 81:6929, 1984; Ausubel et al., *Current Protocols in Molecular Biology*; U.S. Patent Nos. 5,122,463, 5,173,403, 5,187,153, 5,204,254,
15 5,212,058, 5,212,286, 5,215,907, 5,220,013, 5,223,483, and 5,229,279). Plasmid pKK has been modified by replacement of the ampicillin resistance marker gene, by digestion with *Eco*RI, with a kanamycin resistance cassette with *Eco*RI sticky ends (purchased from Pharmacia; obtained from pUC4K, *see, e.g.*, Vieira et al. (*Gene* 19:259-268, 1982; and U.S. Patent No. 4,719,179) into the ampicillin resistance marker
20 gene.

Baculovirus vectors, such as a pBlueBac (also called pJVETL and derivatives thereof) vector, particularly pBlueBac III, (*see, e.g.*, U.S. Patent Nos. 5,278,050, 5,244,805, 5,243,041, 5,242,687, 5,266,317, 4,745,051, and 5,169,784; available from Invitrogen, San Diego) may also be used for expression of the
25 polypeptides in insect cells. The pBlueBacIII vector is a dual promoter vector and provides for the selection of recombinants by blue/white screening as this plasmid contains the β -galactosidase gene (*lacZ*) under the control of the insect recognizable ETL promoter and is inducible with IPTG. A DNA construct may be made in baculovirus vector pBluebac III (Invitrogen, San Diego, CA) and then co-transfected
30 with wild type virus into insect *Spodoptera frugiperda* cells (sf9 cells: *see, e.g.*, Luckow et al., *Bio/technology* 6:47-55, 1988, and U.S. Patent No. 4,745,051).

Other plasmids include the pIN-IIIompA plasmids (*see*, U.S. Patent No. 4,575,013 to Inouye; *see, also*, Duffaud et al., *Meth. Enz.* 153:492-507, 1987), such as pIN-IIIompA2. The pIN-IIIompA plasmids include an insertion site for heterologous
35 DNA linked in transcriptional reading frame with four functional fragments derived from the lipoprotein gene of *E. coli*. The plasmids also include a DNA fragment coding for the signal peptide of the ompA protein of *E. coli*, positioned such that the desired

polypeptide is expressed with the ompA signal peptide at its amino terminus, thereby allowing efficient secretion across the cytoplasmic membrane. The plasmids further include DNA encoding a specific segment of the *E. coli* lac promoter-operator, which is positioned in the proper orientation for transcriptional expression of the desired polypeptide, as well as a separate functional *E. coli* lacI gene encoding the associated repressor molecule that, in the absence of lac operon inducer, interacts with the lac promoter-operator to prevent transcription therefrom. Expression of the desired polypeptide is under the control of the lipoprotein (lpp) promoter and the lac promoter-operator, although transcription from either promoter is normally blocked by the repressor molecule. The repressor is selectively inactivated by means of an inducer molecule thereby inducing transcriptional expression of the desired polypeptide from both promoters.

A particularly preferred vector for expressing VEGF protein is pP_L-λ (Pharmacia Biotech, Uppsala, Sweden). This vector contains the tightly regulated leftward promoter of bacteriophage λ, which is controlled by the cI repressor. The promoter is temperature-inducible by using a bacterial host strain, such as N4830-1, containing the temperature-sensitive cI857 repressor. The vector contains a unique *Hpa*I site for cloning. *Hpa*I digestion leaves blunt ends. The VEGF or VEGF-cytotoxic agent, such as VEGF-SAP, is prepared as a blunt-end fragment (see Examples) and ligated into pP_L-λ. Inclusion bodies containing the protein are isolated, solubilized and refolded.

Preferably, the DNA fragment is replicated in bacterial cells, preferably in *E. coli*. The preferred DNA fragment also includes a bacterial origin of replication, to ensure the maintenance of the DNA fragment from generation to generation of the bacteria. In this way, large quantities of the DNA fragment can be produced by replication in bacteria. Preferred bacterial origins of replication include, but are not limited to, the f1-ori and colE1 origins of replication. Preferred hosts contain chromosomal copies of DNA encoding T7 RNA polymerase operably linked to an inducible promoter, such as the lacUV promoter (see, U.S. Patent No. 4,952,496). Such hosts include, but are not limited to, lysogenic *E. coli* strains HMS174(DE3)pLysS, BL21(DE3)pLysS, HMS174(DE3) and BL21(DE3). Strain BL21(DE3) is preferred. The pLys strains provide low levels of T7 lysozyme, a natural inhibitor of T7 RNA polymerase.

The DNA fragments provided may also contain a gene coding for a repressor-protein. The repressor-protein is capable of repressing the transcription of a promoter that contains sequences of nucleotides to which the repressor-protein binds. The promoter can be derepressed by altering the physiological conditions of the cell.

The alteration can be accomplished by the addition to the growth medium of a molecule that inhibits, for example, the ability to interact with the operator or with regulatory proteins or other regions of the DNA or by altering the temperature of the growth media. Preferred repressor-proteins include, but are not limited to the *E. coli* lacI repressor responsive to IPTG induction, the temperature sensitive cI857 repressor, and the like. The cI857 repressor is particularly preferred.

The DNA construct is introduced into a plasmid suitable for expression in the selected host. The sequences of nucleotides in the plasmids that are regulatory regions, such as promoters and operators, are operationally associated with another for transcription. The sequence of nucleotides encoding the VEGF, VEGF chimera or cytotoxic agent may also include DNA encoding a secretion signal, whereby the resulting peptide is a precursor protein. Secretion signals suitable for use are widely available and are well known in the art. Prokaryotic and eukaryotic secretion signals functional in *E. coli*, may be employed. The presently preferred secretion signals include, but are not limited to, those encoded by the following *E. coli* genes: ompA, ompT, ompF, ompC, beta-lactamase, pelB and bacterial alkaline phosphatase, and the like (von Heijne (1985) *J. Mol. Biol.* 184:99-105). In addition, the bacterial pelB gene secretion signal (Lei et al. (1987) *J. Bacteriol.* 169:4379, 1987), the phoA secretion signal, and the cec2 secretion signal, functional in insect cells, may be employed. The most preferred secretion signal for bacterial expression is the *E. coli* ompT secretion signal. For eukaryotic expression systems, particularly insect cell systems, the signals from secreted proteins, such as insulin, growth hormone, mellitin, and mammalian alkaline phosphatase are of interest herein. Other prokaryotic and eukaryotic secretion signals known to those of skill in the art may also be employed (see, e.g., von Heijne (1985) *J. Mol. Biol.* 184:99-105). Using the methods described herein, one of skill in the art can substitute secretion signals that are functional in either yeast, insect or mammalian cells to secrete the heterologous protein from those cells. The resulting processed protein may be recovered from the periplasmic space or the fermentation medium or growth medium.

In certain preferred embodiments, the constructs also include a transcription terminator sequence. The promoter regions and transcription terminators are each independently selected from the same or different genes. In some embodiments, the DNA fragment is replicated in bacterial cells, preferably in *E. coli*. The DNA fragment also typically includes a bacterial origin of replication, to ensure the maintenance of the DNA fragment from generation to generation of the bacteria. In this way, large quantities of the DNA fragment can be produced by replication in bacteria.

Preferred bacterial origins of replication include, but are not limited to, the fl-ori and col E1 origins of replication.

DNA encoding full-length VEGF, VEGF-SAP, SAP-VEGF with and without linkers, and other such constructs, are introduced into the pET vectors, preferably pET-11a (Novagen, Madison, WI) or the pP_L-λ vector (Pharmacia). It is found that for expression in bacterial hosts that constructs in which DNA encoding SAP is linked, directly or via a linker, to DNA encoding the N-terminus of VEGF is preferred. When the SAP-VEGF₁₂₁ or SAP-VEGF₁₆₅ is produced in pP_L-λ, no linker is preferable. Also, constructs containing DNA encoding two monomers, which upon expression, dimerize, preferably in an antiparallel manner, are preferred.

E. Method of preparation of VEGF-targeted agent conjugates

Conjugates that contain one or more VEGF polypeptides linked, either directly or via a linker, to one or more targeted agents are provided. The presently preferred VEGF monomers are VEGF₁₆₅ and VEGF₁₂₁. VEGF₁₂₁ is particularly preferred.

As described above, the conjugates contain the following components: (VEGF)_n, (L)_q, and (targeted agent)_m in which: at least one VEGF moiety is linked with or without a linker (L) to at least one targeted agent, n is 1 or more, generally is at least 2, and typically is between 2 and 6; q is 0 or more as long as the resulting conjugate binds to the targeted receptor, is internalized and delivers the targeted agent, q is generally 0 or 1 to 4; m is 1 or more, generally 1 or 2; L refers to a linker, and the targeted agent is any agent, such as a cytotoxic agent or a nucleic acid, or a drug, such as methotrexate, intended for internalization by a cell that expresses a receptor to which VEGF binds and upon binding is internalized. The components may be organized in any order.

It is also understood that substitutions in codons by virtue of the degeneracy of the genetic code are encompassed by DNA encoding such VEGF. DNA encoding the VEGF polypeptide may be obtained from any source known to those of skill in the art; it may be isolated using standard cloning methods, synthesized or obtained from commercial sources, prepared as described in any of the patents and publications noted herein.

In some embodiments, the conjugates provided herein may be represented by the formula (I):

(VEGF)_p-(L)_q-(targeted agent)_n

in which VEGF refers to a polypeptide that is reactive with a VEGF receptor (also referred to herein as a VEGF protein), such as VEGF. L refers to a

linker, which may be present or absent, q is 0 or more as long as the resulting conjugate binds to a targeted receptor and the targeted agent is internalized, p is 1 or more, preferably 1, and generally less than or equal to 4, and the targeted agent is any agent, such as a cytotoxic agent or a nucleic acid, or a drug, such as methotrexate, intended for internalization by a cell that expresses a VEGF receptor; n is 1 or 2; and the VEGF may be linked to the linker or targeted agent via its N-terminus or C-terminus or any other locus in polypeptide, such as derivatized cys residues. When n is 2, the conjugates are linked via cysteine residues on the VEGF, probably via residues that correspond to the cysteines at positions 77 and 86 in SEQ ID NOs. 25-28. The linked VEGFs may be linked in a parallel fashion or antiparallel fashion. Conjugates of the formula (II): targeted agent-L-(VEGF)_n, in which n is 1 or 2, are also provided. These conjugates are prepared by mixing conjugates of formula I with unconjugated VEGF, by preparing fusion proteins from DNA constructs that encode two VEGF moieties, or by mixing conjugates of formulas I and II. The VEGF moieties are preferably linked via a linker to facilitate dimerization.

It is understood that the VEGF and targeted agent (or linker and targeted agent) may be linked in any order and through any appropriate linkage, as long as the resulting conjugate binds to a receptor to which VEGF binds and internalizes the targeted agent(s) in cells bearing the receptor.

For example, the VEGF polypeptide may be linked to the targeted agent or linker at or near its N-terminus or at or near its C-terminus. The VEGF may be linked to a second VEGF monomer, which may be the same monomer or a different monomer; and one or more targeted agents that are the same or different may be linked to the VEGF or may be linked to each other. The linkage may be at any locus, although the N-terminus region of VEGF (within about 20, preferably 10, amino acids from the N-terminus) is preferred. When multiple VEGFs are linked, they may be in a head to head, head to tail or tail to tail orientation. If more than one targeted agent is included, the second may be the same or different from the first agent. In order to efficiently bind to VEGF receptors and deliver a targeted agent to a cell, VEGF dimerization appears to be required.

In addition, conjugates in which non-essential cysteines in the VEGF monomers and/or targeted agent, if the agent is a polypeptide, are deleted or replaced with Ser or other conservative substitution are provided. Compositions of such conjugates should exhibit reduced aggregation compared to conjugates that contain non-essential cysteines. Non-essential cysteines may be identified empirically.

Polypeptides that are reactive with a VEGF receptor (VEGF proteins) include any molecule that reacts with VEGF receptors on cells that bear VEGF

receptors and results in internalization of the linked cytotoxic agent. Particularly preferred polypeptides that are reactive with a VEGF receptor include members of the VEGF family of polypeptides, muteins of these polypeptides, chimeric or hybrid molecules that contain portions of any of these family members, and any portion thereof that binds to VEGF receptors and internalizes a linked agent.

The linker is selected to increase the specificity, toxicity, solubility, serum stability, and/or intracellular availability targeted moiety. More preferred linkers are those that can be incorporated in fusion proteins and expressed in a host cell, such as *E. coli*. Such linkers include: enzyme substrates, such as cathepsin B substrate, cathepsin D substrate, trypsin substrate, thrombin substrate, subtilisin substrate, factor Xa substrate, and enterokinase substrate; linkers that increase solubility, flexibility, and/or intracellular cleavability, such as $(\text{gly}_m\text{ser})_n$ and $(\text{ser}_m\text{gly})_n$, in which n is 1 to 6, preferably 1 to 4, most preferably 1, and m is 1 to 6, preferably 1 to 4, more preferably 12 to 4, most preferably. Preferred among such linkers, are those, such as cathepsin D substrate, that are preferentially cleaved in the endosome or cytoplasm following internalization of the conjugate linker; other such linkers, such as $(\text{gly}_m\text{ser})_n$ and $(\text{ser}_m\text{gly})_n$, also increase the flexibility, serum stability and/or solubility of the conjugate or the availability of the region joining the VEGF and targeted agent for cleavage. In some embodiments, several linkers that are the same or different may be included in order to take advantage of desired properties of each linker.

Other linkers are suitable for incorporation into chemically produced conjugates. Linkers that are suitable for chemically linking conjugates include disulfide bonds, thioether bonds, hindered disulfide bonds, and covalent bonds between free reactive groups, such as amine and thiol groups. These bonds are produced using heterobifunctional reagents to produce reactive thiol groups on one or both of the polypeptides and then reacting the thiol groups on one polypeptide with reactive thiol groups or amine groups to which reactive maleimido groups or thiol groups can be attached on the other. Other linkers include acid cleavable linkers, such as bismaleimideoxy propane, acid labile-transferrin conjugates and adipic acid dihydrazide, that would be cleaved in more acidic intracellular compartments and cross linkers that are cleaved upon exposure to UV or visible light and linkers.

The targeted agents or moieties include any molecule that, when internalized, alter the metabolism or gene expression in the cell. Such agents include cytotoxic agents, such as ribosome inactivating proteins DNA encoding cytotoxic agents, and antisense nucleic acids, that result in inhibition of growth or cell death. Other such agents also include antisense RNA, DNA, and truncated proteins that alter gene expression via interactions with the DNA, or co-suppression or other mechanism.

The conjugates herein may also be used to deliver DNA and thereby serve as agents for gene therapy or to deliver agents that, upon, transcription and/or translation thereof, result in cell death. Cytotoxic agents include, but are not limited to, ribosome inactivating proteins, inhibitors of DNA, RNA and/or protein synthesis, including antisense nucleic acids, and other metabolic inhibitors. In certain embodiments, the cytotoxic agent is a ribosome-inactivating protein (RIP), such as, for example, saporin, although other cytotoxic agents can also be advantageously used.

The targeted agents may also be modified to render them more suitable for conjugation with the linker and/or a VEGF protein or to increase their intracellular activity. Such modifications include, but are not limited to, the introduction of a Cys residue at or near the N-terminus or C-terminus, derivatization to introduce reactive groups, such as thiol groups, and addition of sorting signals, such as (XaaAspGluLeu)_n (SEQ ID NO. 50), where Xaa is Lys or Arg, preferably Lys, and n is 1 to 6, preferably 1-3, at, preferably, the carboxy-terminus (*see, e.g.*, Seetharam et al. (1991) *J. Biol. Chem.* 266:17376-17381; and Buchner et al. (1992) *Anal. Biochem.* 205:263-270), that direct the targeted agent to the endoplasmic reticulum or the addition of a cytoplasmic sorting sequence, such as KDEL (see discussion herein).

Conjugates that contain a plurality of monomers of a VEGF protein linked to the cytotoxic agent are also provided. These conjugates that contain several, typically two to about six monomers can be produced by linking multiple copies of DNA encoding the VEGF fusion protein, typically head-to-tail, under the transcriptional control of a single promoter region. In addition conjugates that contain, more than one targeted agent per VEGF, such as SAP-VEGF-SAP, linked with or without linkers are contemplated herein.

1. Chemical conjugation

a. Preparation of VEGF polypeptides for chemical conjugation

VEGF may be isolated from a suitable source or may be produced using recombinant DNA methodology, discussed below. As used herein, substantially pure means sufficiently homogeneous to appear free of readily detectable impurities as determined by standard methods of analysis, such as thin layer chromatography (TLC), gel electrophoresis, high performance liquid chromatography (HPLC), used by those of skill in the art to assess such purity, or sufficiently pure such that further purification would not detectably alter the physical and chemical properties, such as enzymatic and biological activities, of the substance. Methods for purification of the compounds to produce substantially chemically pure compounds are known to those of skill in the art. A substantially chemically pure compound may, however, be a mixture of

stereoisomers. In such instances, further purification might increase the specific activity of the compound.

To effect chemical conjugation herein, the VEGF protein is conjugated generally via a reactive amine group or thiol group to the targeted agent or to a linker, which has been or is subsequently linked to the targeted agent. The VEGF protein is conjugated either via its N-terminus, C-terminus, or elsewhere in the polypeptide. In preferred embodiments, the VEGF protein is conjugated via a reactive cysteine residue to the linker or to the targeted agent. The VEGF can also be modified by addition of a cysteine residue, either by replacing a residue or by inserting the cysteine, at or near the amino or carboxyl terminus, within about 20, preferably 10 residues from either end, and preferably at or near the amino terminus.

In preferred embodiments, to reduce the heterogeneity of preparations, the VEGF protein is modified by mutagenesis to replace reactive cysteines, leaving, preferably, only one available cysteine for reaction. The VEGF protein is modified by deleting or replacing a site(s) on the VEGF that causes the heterogeneity. Such sites are typically cysteine residues that, upon folding of the protein, remain available for interaction with other cysteines or for interaction with more than one cytotoxic molecule per molecule of VEGF peptide. Thus, such cysteine residues do not include any cysteine residue that are required for proper folding of the VEGF peptide or for retention of the ability to bind to a VEGF receptor and internalize. For chemical conjugation, one cysteine residue that, in physiological conditions, is available for interaction, is not replaced because it is used as the site for linking the cytotoxic moiety. The resulting modified VEGF is conjugated with a single species of cytotoxic conjugate.

Alternatively, the contribution of each cysteine to the ability to bind to VEGF receptors may be determined empirically, as described above. Recently the role of Cys-25, Cys-56, Cys-67, Cys-101, and Cys 145 in dimerization and biological activity was assessed (Claffery, *supra*). Cys-25, Cys-56, and Cys-67 are required for dimerization; Cys-101 is required for expression. Substitution of Cys-145 is preferred.

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b. Preparation of targeted proteins for chemical conjugation

If the targeted agent is a polypeptide it may be directly linked to the VEGF or VEGF with linker or to a linker by reaction of a reactive group in the polypeptide. It is desirable, however, that the agent may react at only a single locus, so that the resulting preparation of conjugates is homogeneous. Thus, if necessary, the targeted agent can be derivatized and then a single species isolated. Alternatively, and preferably for chemical conjugation, saporin can be modified so that it only has one

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reactive group, such as a cysteine, for a particular set of conditions and reagents. For example, saporin has been derivatized and a single species isolated and has also been modified by introduction of a single cysteine residue.

Saporin for chemical conjugation may be produced by isolating the
5 protein from the leaves or seeds of *Saponaria officinalis* or using recombinant methods and the DNA provided herein or known to those of skill in the art or obtained by screening appropriate libraries (*see, e.g.*, International PCT Application WO 93/25688, which describes the isolation of saporin, plasmids containing DNA encoding saporin, expression of saporin and isolation of purified saporin). Some DNA encoding saporin
10 may also include an N-terminal extension sequence linked to the amino terminus of the saporin that encodes a linker so that, if desired, the SAP and linker can be expressed as a fusion protein as described herein. The sequence of DNA encoding saporin is set forth in SEQ ID Nos. 3-7.

The DNA molecules provided herein encode saporin that has
15 substantially the same amino acid sequence and ribosome-inactivating activity as that of saporin-6 (SO-6), including any of four isoforms, which have heterogeneity at amino acid positions 48 and 91 (*see, e.g.*, Maras et al. (1990) *Biochem. Internat.* 21:631-638 and Barra et al. (1991) *Biotechnol. Appl. Biochem.* 13:48-53 and SEQ ID NOs. 3-7). Other suitable saporin polypeptides include other members of the multi-gene family
20 coding for isoforms of saporin-type RIPs including SO-1 and SO-3 (Fordham-Skelton et al. (1990) *Mol. Gen. Genet.* 221:134-138), SO-2 (*see, e.g.*, U.S. Application Serial No. 07/885,242, which corresponds to GB 2,216,891; *see, also*, Fordham-Skelton et al. (1991) *Mol. Gen. Genet.* 229:460-466), SO-4 (*see, e.g.*, GB 2,194,241 B; *see, also*, Lappi et al. (1985) *Biochem. Biophys. Res. Commun.* 129:934-942) and SO-5 (*see, e.g.*,
25 GB 2,194,241 B; *see, also*, Montecucchi et al. (1989) *Int. J. Peptide Protein Res.*, 33:263-267; and Ferreras et al. (1993) *Biophys. Biochem. Acta* 1216:31-42). SO-4, which includes the N-terminal 40 amino acids set forth in SEQ ID NO. 77, is isolated from the leaves of *Saponaria officinalis* by extraction with 0.1 M phosphate buffer at pH 7, followed by dialysis of the supernatant against sodium borate buffer, pH 9, and
30 selective elution from a negatively charged ion exchange resin, such as Mono S (Pharmacia Fine Chemicals, Sweden) using a gradient of 1 to 0.3 M NaCl and is the first eluting chromatographic fraction that has SAP activity. The second eluting fraction is SO-5.

Because more than one amino group on SAP may react with the
35 succinimidyl moiety, it is possible that more than one amino group on the surface of the protein is reactive. This creates the potential for heterogeneity even if mono-derivatized SAP is used. This source of heterogeneity has been solved by the

conjugating modified SAP expressed in *E. coli* that has an additional cysteine inserted in the coding sequence, preferably within 10 or 20 amino acids of either the C-terminus or N-terminus. The preferred molecule has the Met-Cys inserted at the N-terminus.

As discussed above, muteins of saporin that contain a Cys at or near the amino or carboxyl terminus can be prepared. Thus, instead of derivatizing saporin to introduce a sulfhydryl, the saporin can be modified by the introduction of a cysteine residue into the SAP such that the resulting modified saporin protein reacts with a VEGF monomer or a linker (and then to a VEGF monomer) to produce a conjugate. It is understood that, as discussed above and below, in order for the cytotoxic conjugates herein to bind to VEGF receptors most effectively, the VEGF portion of the conjugate should be dimerized.

Preferred loci for introduction of a cysteine residue include the N-terminus region, preferably within about one to twenty residues, more preferably one to about ten residues, from the N-terminus of the cytotoxic agent, such as SAP. For expression of SAP in the bacterial host systems herein, it is also desirable to add DNA encoding a methionine linked to the DNA encoding the N-terminus of the saporin protein. DNA encoding SAP has been modified by inserting a DNA encoding Met-Cys (ATG TGT or ATG TGC) at the N-terminus immediately adjacent to the codon for first residue of the mature protein.

Muteins in which a cysteine residue has been added at the N-terminus and muteins in which the amino acid at position 4 or 10 has been replaced with cysteine have been prepared by modifying the DNA encoding saporin (see, Examples). Preferably, saporin has a cysteine added at the -1 position (see Example 3). The modified DNA may be expressed and the resulting saporin protein purified, as described herein for expression and purification of the resulting SAP. The modified saporin can then be reacted with a VEGF, preferably a VEGF dimer, to form disulfide linkages between the VEGF dimer and the cysteine residue on the modified SAP.

Typically, SAP is derivatized by reaction with SPDP. This results in a heterogeneous population. For example, SAP that is derivatized by SPDP to a level of 0.9 moles pyridine-disulfide per mole of SAP includes a population of non-derivatized, mono-derivatized and di-derivatized SAP. Methods for isolation of mono-derivatized saporin are described, for example, in Lappi et al. (1993) *Anal. Biochem.* 212:446-451, copending U.S. Application Serial No. 08/099,924). The methods rely on the charge differences among the three species of SAP that are produced upon reaction of one or more lysines in saporin with SPDP. The mono-derivatized saporin species is purified by Mono-S cation exchange chromatography and pooling of the fractions that contain the monoderivatized species. Briefly, the initial eluting peak is composed of SAP that

is approximately di-derivatized; the second peak is mono-derivatized and the third peak shows no derivatization. The di-derivatized material accounts for 20% of the three peaks; the second accounts for 48% and the third peak contains 32%. Fractions that have a ratio of SPDP to SAP greater than 0.85 but less than 1.05 are pooled, dialyzed
5 against an appropriate buffer, such as 0.1 M sodium chloride, 0.1 M sodium phosphate, pH 7.5, used for coupling to a linker, to a VEGF monomer, a VEGF dimer, a VEGF monomer with linker, or a VEGF dimer with linker.

The resulting preparation, although more uniform, still contains some heterogeneity because native saporin as purified from the seed is a mixture of four
10 isoforms, as judged by protein sequencing (*see, e.g.*, PCT Application WO 93/25688 (Serial No. PCT/US93/05702), United States Application Serial No. 07/901,718; *see also*, Montecucchi et al. (1989) *Int. J. Pept. Prot. Res.* 33:263-267; Maras et al. (1990) *Biochem. Internat.* 21:631-638; and Barra et al. (1991) *Biotechnol. Appl. Biochem.* 13:48-53). This creates some heterogeneity in the conjugates, since the reaction with
15 SPDP probably occurs equally within each isoform. This source of heterogeneity can be removed by using saporin expressed in *E. coli*.

c. Chemical conjugation of a VEGF protein to linkers and targeted agents

The VEGF monomers are preferably linked via non-essential cysteine
20 residues to the linkers or to the targeted agent. VEGF that has been modified by introduction of a Cys residue at or near one terminus, preferably the N-terminus is preferred for use in chemical conjugation (see Examples for preparation of such modified VEGF). For use herein, the VEGF, preferably, is dimerized prior to linkage
25 to the linker and/or targeted agent. Methods for coupling proteins to the linkers, such as the heterobifunctional agents, or to nucleic acids, or to proteins are known to those of skill in the art and are also described herein.

Methods for chemical conjugation of proteins are known to those of skill in the art. The preferred methods for chemical conjugation depend on the selected
30 components, but preferably rely on disulfide bond formation. For example, if the targeted agent is SPDP-derivatized saporin, then it is advantageous to dimerize the VEGF moiety prior coupling or conjugating to the derivatized saporin.

2. Fusion protein of a VEGF polypeptide and targeted agent

35 Expression of DNA encoding a fusion of a VEGF protein linked to the targeted agent results in a more homogeneous preparation of cytotoxic conjugates and is suitable for use, when the selected targeting agent and linker are polypeptides.

Aggregate formation may be reduced in preparations containing the fusion proteins by modifying the VEGF, particularly, VEGF₁₆₅, VEGF₁₈₉ and VEGF₂₀₆, which contain nonessential cysteines in the heparin binding domain and/or the targeted agent to prevent cysteine-cysteine interactions between each conjugate or decrease secondary structure.

a. Expression of VEGF

DNA encoding VEGF peptides and/or the amino acid sequences of VEGFs are known to those of skill in this art (*see, e.g.*, SEQ ID NOs. 18-28). DNA may be prepared synthetically based on the amino acid sequence or known DNA sequence of a VEGF or may be isolated using methods known to those of skill in the art or obtained from commercial or other sources known to those of skill in this art.

It is also understood that substitutions in codons by virtue of the degeneracy of the genetic code are encompassed by DNA encoding such VEGF. DNA encoding the VEGF polypeptide may be obtained from any source known to those of skill in the art; it may be isolated using standard cloning methods, synthesized or obtained from commercial sources, prepared as described in any of the patents and publications noted herein.

Such DNA may then be mutagenized using standard methodologies to delete, replace any cysteine residues, as described herein, that are not required for dimerization and receptor binding and internalization, or insert cysteine residues for chemical conjugation (*see*, SEQ ID NOs. 86-89). As necessary, the identity of non-essential cysteine residues may be determined empirically, by deleting, inserting and/or replacing a cysteine residue and ascertaining whether the resulting VEGF with the deleted cysteine form aggregates in solutions containing physiologically acceptable buffers and salts. Loci for insertion of cysteine residues may also be determined empirically. Generally, regions at or near (within 20, preferably 10 amino acids) the C- or, preferably, the N-terminus.

As discussed above, binding to a VEGF receptor followed by internalization are the activities required for a VEGF protein to be suitable for use herein. A test of such activity, which reflects the ability to bind to VEGF receptors and to be internalized, is the ability of a conjugate containing VEGF (*e.g.*, VEGF-saporin) to inhibit proliferation of cells, such as vascular endothelial cells, including bovine or human aortic endothelial cells, that bear VEGF receptors. Any VEGF polypeptide that possesses such ability is intended for use herein.

The DNA encoding the conjugate can be inserted into a plasmid and expressed in a selected host. Multiple copies of the DNA encoding the VEGF-targeted

agent chimera or VEGF-cytotoxic agent chimera can be inserted into a single plasmid in operative linkage with one promoter. When expressed, the resulting protein will be a VEGF-cytotoxic agent multimer. Typically two to six copies of the chimera are inserted into a plasmid, preferably in a head to tail orientation. Alternatively, one or more copies of the VEGF-targeted agent chimera is inserted under the control of a first promoter in a plasmid and one or more copies encoding a VEGF polypeptide is inserted under the control of a second promoter in the plasmid or into a second plasmid. The resulting plasmid(s) is (are) introduced into a host and cultured under conditions in which the promoter is active and the conjugated and a VEGF polypeptide are produced. The resulting preparation is treated to permit refolding of the VEGF and dimerization. Conjugates containing VEGF dimers are isolated.

b. Preparation of muteins for recombinant production of the conjugates

For recombinant expression using the methods herein, all cysteines in the VEGF peptide that are not required for biological activity can be deleted or replaced; and for use in the chemical conjugation methods herein, all except for one of these cysteines, which will be used for chemical conjugation to the cytotoxic agent, can be deleted or replaced. Human (and the corresponding bovine protein) VEGF₁₂₁ has nine cysteine residues and VEGF₁₆₅ and VEGF₁₈₉ have 16 cysteine residues per monomer. Each of the nine cysteines may be replaced and the resulting mutein tested for the ability to bind to VEGF receptors and to be internalized as described herein. Alternatively, the resulting mutein-encoding DNA is used as part of a construct containing DNA encoding the cytotoxic agent linked to the VEGF-encoding DNA. The construct is expressed in a suitable host cell and the resulting protein tested for the ability to bind to VEGF receptors and internalize the cytotoxic agent. As long this ability is retained the mutein is suitable for use herein.

c. DNA constructs and expression of the constructs

DNA encoding VEGF conjugates is expressed in any suitable host, particularly bacterial and insect hosts. Methods and plasmids for such expression are set forth in the examples (see, also Table 3).

Using the methods and materials described above and in the examples numerous chemical conjugates and fusion proteins have been synthesized. These include the constructs set forth in Table 3, below.

Particular details of the syntheses of the constructs are set forth in the EXAMPLES. The constructs have been synthesized and have been or can be inserted

into plasmids including pET 11 (with and without the T7 transcription terminator), pET 12 and pET 15 (Invitrogen, San Diego), pP_L-λ and pKK223-3 (Pharmacia, P.L.) and derivatives of pKK223-3. The resulting plasmids have been and can be transformed into bacterial hosts including BL21, BL21(DE3), HMS174(DE3), (Novagen, Madison, WI) and N4830(cI857) (see, Gottesman et al. (1980) *J. Mol. Biol.* 140:57-75, commercially available from PL Biochemicals, Inc., also, *see, e.g.*, U.S. Patent Nos. 5,266,465, 5,260,223, 5,256,769, 5,256,769, 5,252,725, 5,250,296, 5,244,797, 5,236,828, 5,234,829, 5,229,273, 4,798,886, 4,849,350, 4,820,631 and 4,780,313) or N99CI⁺ for pP_L-λ. N4830 harbors a heavily deleted phage lambda prophage carrying the mutant cI857 temperature sensitive repressor and an active N gene. The constructs have also been introduced in baculovirus vector sold commercially under the name pBlueBacIII (Invitrogen, San Diego CA; see the Invitrogen catalog; see, also, Vialard et al. (1990) *J. Virol.* 64:37; U.S. Patent No. 5,270,458; U.S. Patent No. 5,243,041; and published International PCT Application WO 93/10139, which is based on U.S. patent application Serial No. 07/792,600. The pBlueBacIII vector is a dual promoter vector and provides for the selection of recombinants by blue/white screening as this plasmid contains the β-galactosidase gene (lacZ) under the control of the insect recognizable ETL promoter and is inducible with IPTG. The baculovirus vector is then co-transfected with wild type virus into insect host cells *Spodoptera frugiperda* (sf9; *see, e.g.*, Luckow et al. (1988) *Bio/technology* 6:47-55 and U.S. Patent No. 4,745,051).

TABLE 3

Plasmid(s)***	Description of Fusion Protein	Fusion Protein Name
PZ50B1	SAP CYS-1	FPS1
PZ51B1	SAP CYS+4	FPS2
PZ51E1	SAP CYS+4	FPS2
PZ52B1	SAP CYS+10	FPS3
PZ52E1	SAP CYS+10	FPS3
PZ70B1	VEGF ₁₆₅ (-signal seq.)	FPV1
PZ71B1	VEGF ₁₆₅ (+signal seq.)	FPV1
PZ115B1	VEGF ₁₂₁ (+signal seq.)	
PZ116B1	VEGF ₁₂₁ (-signal seq.)	
PZ72B1	VEGF ₁₆₅ -AlaMet-SAP (-signal seq.)	FPVS1
PZ73B1	VEGF ₁₆₅ -AlaMet-SAP (+signal seq.)	FPVS1
PZ74B1	SAP-AlaMet-VEGF ₁₆₅	FPSV1
PZ74F5	SAP-AlaMet-VEGF ₁₆₅	FPSV1

PZ75B1	SAP-(Gly4Ser)4-VEGF ₁₆₅	FPSV2
PZ75F5	SAP-(Gly4Ser)4-VEGF ₁₆₅	FPSV2
PZ76B1	SAP-AlaMet-VEGF ₁₂₁	FPSV3
PZ76F5	SAP-AlaMet-VEGF ₁₂₁	FPSV3
PZ77B1	SAP-G4Sx4-VEGF ₁₂₁	FPSV4
PZ78F5	SAP-G4Sx4-VEGF ₁₂₁	FPSV4
PZ79B1	SAP-AlaMet-VEGF ₁₂₁ (Gly4Ser)-VEGF ₁₂₁	FPSVV1
PZ79F5	SAP-AlaMet-VEGF ₁₂₁ (GlySer)-VEGF ₁₂₁	
PZ80B1	SAP-AlaMet-VEGF ₁₂₁ (Gly4Ser) ₂ -VEGF ₁₂₁	FPSVV2
PZ81B1	SAP-AlaMet-VEGF ₁₆₅ (Gly4Ser)-VEGF ₁₆₅	FPSVV3
PZ81F5	SAP-AlaMet-VEGF ₁₆₅ (GlySer)-VEGF ₁₆₅	
PZ82B1	SAP-AlaMet-VEGF ₁₆₅ (Gly4Ser) ₂ -VEGF ₁₆₅	FPSVV4
PZ83B1	SAP-(Gly4Ser)-VEGF ₁₂₁ (Gly4Ser)-VEGF ₁₂₁	FPSVV5
PZ84B1	SAP-(Gly4Ser) ₂ -VEGF ₁₂₁ (Gly4Ser) ₂ -VEGF ₁₂₁	FPSVV6
PZ85B1	SAP-(Gly4Ser)-VEGF ₁₆₅ (Gly4Ser)-VEGF ₁₆₅	FPSVV7
PZ85F5	SAP-(GlySer)-VEGF ₁₆₅ (Gly4Ser)-VEGF ₁₆₅	
PZ86B1	SAP-(Gly4Ser) ₂ -VEGF ₁₆₅ (Gly4Ser) ₂ -VEGF ₁₆₅	FPSVV8
PZ87I	VEGF ₁₂₁ (Baculovirus) Viral Stock	FPV2
PZ87I7	VEGF ₁₂₁	FPV2
PZ88I	VEGF ₁₆₅ (Baculovirus) Viral Stock	FPV1
PZ88I7	VEGF ₁₆₅	FPV1
PZ89I	VEGF ₁₂₁ CYS+2(Baculovirus) Viral Stock	FPV3
PZ89I7	VEGF ₁₂₁ CYS+2	FPV3
PZ90I	VEGF ₁₂₁ CYS+4(Baculovirus) Viral Stock	FPV4
PZ90I7	VEGF ₁₂₁ CYS+4	FPV4
PZ91I	VEGF ₁₆₅ CYS+2(Baculovirus) Viral Stock	FPV5
PZ91I	VEGF ₁₆₅ CYS+2	FPV5
PZ92I	VEGF ₁₆₅ CYS+4 (BACULOVIRUS) Viral Stock	FPV6
PZ92I7	VEGF ₁₆₅ CYS+4	FPV6
PZ93F5	Met VEGF ₁₂₁	FPV2
PZ94F5	Met VEGF ₁₆₅	FPV1
PZ95B1	pel B-SAP-AlaMet-V ₁₂₁ -(G45)-V ₁₂₁	FPSVV1
PZ96B1	ompA-SAP-AlaMet-V ₁₂₁ -(G45)-V ₁₂₁	FPSVV1
PZ97B1	ompT-SAP-AlaMet-V ₁₂₁ -(G45)-V ₁₂₁	FPSVV1
PZ98B1	phoA-SAP-AlaMet-V ₁₂₁ -(G45)-V ₁₂₁	FPSVV1
PZ99B1	pelB-SAP-AlaMet-V ₁₆₅ -(G45)-V ₁₆₅	FPSVV3
PZ100B1	ompA-SAP-AlaMet-V ₁₆₅ -(G45)-V ₁₆₅	FPSVV3
PZ101B1	ompT-SAP-AlaMet-V ₁₆₅ -(G45)-V ₁₆₅	FPSVV3
PZ102B1	phoA-SAP-AlaMet-V ₁₆₅ -(G45)-V ₁₆₅	FPSVV3
PZ103B1	SAP-VEGF exon 3.4.5	FPSV5
PZ104B1	SAP-VEGF exon 6.7.8	FPSV7

PZ105B1	SAP-VEGF exon 3,4,5,6	
PZ106I1	pMAL-p2=I SAP-VEGF exon 3,4,5	FPSV5
PZ107I1	pMAL-p2=I SAP-VEGF exon 3,4,5,6	FPSV6
PZ108I1	pMAL-p2=I SAP-VEGF exon 6,7,8	FPSV7
PZ111J1	PGEX-SX=SAP VEGF exon 3,4,5	FPSV5
PZ112J1	PGEX-SX=SAP VEGF exon 3,4,5,6	FPSV6
PZ113J1	PGEX-SX=SAP VEGF exon 7,8	FPSV8
PZ114J1	PGEX-SX=SAP VEGF exon 6,7,8	FPSV7

* Details regarding these constructs are described in co-pending U.S. Application Serial Nos. 08/213,446 and 08/213,446, International PCT Application WO 53189, and PCT Appln. US 94/ , filed July 27, 1994

5 ** N/A = not applicable

*** The plasmids, such as PZ1A1 are designated with (i) a PZnumber (PZ1), followed by (ii) a letter (A), and optionally (iii) followed by a number (1). The key to these designations: (i) PZnumber - refers to the construct number, (ii) the next letter refers to the plasmid into which the construct was cloned, A=pET 11 without the T7 transcription terminator, B=pET 11 with the T7 transcription terminator, c=pET 13, D=pET 12, E=pET 15b, F=pPL λ , G=pKK 223-3, H=PRZ 1 (pKK223-3+Kan^R), I=pBlueBac III, J=PRZ2 (pKK223-3 + Kan^R + lacI gene) and (ii) the optional number (or letter) refers to the bacterial strain (number) or insect host (letter) in which the plasmid was introduced, 1=BL21(DE3), 2=BL21(DE3)+pLYS S; 3=HMS174(DE3), 4=HMS174(DE3)+pLYS S, 5=N4830(cI8576) and 7=NovaBlue.

A particularly preferred vector for expressing VEGF or VEGF-cytotoxic agent fusion protein is pP_L- λ inducible expression vector (Pharmacia Biotech, Uppsala, Sweden). As described above, this vector contains the tightly regulated leftward promoter of bacteriophage λ , which is controlled by the cI repressor. The promoter is temperature inducible in a bacterial host, such as N4830-1, which contains the ts repressor cI857. Upon induction, the expressed protein is expressed and compartmentalized into inclusion bodies. The inclusion bodies are released by lysing the cells, such as with lysozyme digestion and sonication. The insoluble fraction, containing the inclusion bodies, is isolated by centrifugation. The inclusion bodies are solubilized by a strong denaturant, such as 6M guanidine-HCl or urea. The proteins are recovered from the supernatant following centrifugation by dilution into a buffer containing 100mM Tris, 10mM EDTA, 1% monothioglycerol 0.25M L-arginine, pH9.5. Other equivalent components may be readily substituted as long as the pH is basic and a reduction agent is present. The dilution is performed slowly and the

mixture stirred for up to 2 hours. Refolding the protein is accomplished by dialysis of the protein into buffer, such as PBS, pH 8.8.

F. Properties and use of the resulting chemical conjugates and fusion proteins

5 The conjugates provided herein can be used *in vitro* to identify cells, particularly tumor cells that express receptors to which the conjugate selectively binds and which internalized the conjugates. The cells are contacted with the conjugates and assayed for proliferation. Cells in which proliferation is inhibited express VEGF receptors. If such cells are derived from a tumor, such tumor will be a candidate for
10 treatment with the VEGF conjugate. If such cells are a cell line, such cell line will be useful in drug screening assays for identification of compounds that modulate the activity of VEGF receptors (*see, e.g.*, U.S. Patent Nos. 5,208,145, 5,071,773, 4,981,784, 4,603,106, which describe such assays for other receptors).

15 **G. Formulation and administration of pharmaceutical compositions**

 The conjugates herein may be formulated into pharmaceutical compositions suitable for topical, local, intravenous and systemic application. Effective concentrations of one or more of the conjugates are mixed with a suitable pharmaceutical carrier or vehicle. The concentrations or amounts of the conjugates that
20 are effective requires delivery of an amount, upon administration, that ameliorates the symptoms or treats the disease. Typically, the compositions are formulated for single dosage administration. Therapeutically effective concentrations and amounts may be determined empirically by testing the conjugates in known *in vitro* and *in vivo* systems, such as those described here; dosages for humans or other animals may then be
25 extrapolated therefrom.

 Upon mixing or addition of the conjugate(s) with the vehicle, the resulting mixture may be a solution, suspension, emulsion or the like. The form of the resulting mixture depends upon a number of factors, including the intended mode of administration and the solubility of the conjugate in the selected carrier or vehicle. The
30 effective concentration is sufficient for ameliorating the symptoms of the disease, disorder or condition treated and may be empirically determined based upon *in vitro* and/or *in vivo* data, such as the data from the mouse xenograft model for tumors or rabbit ophthalmic model. If necessary, pharmaceutically acceptable salts or other derivatives of the conjugates may be prepared.

35 Pharmaceutical carriers or vehicles suitable for administration of the conjugates provided herein include any such carriers known to those skilled in the art to

be suitable for the particular mode of administration. As used herein, pharmaceutically acceptable salts, esters or other derivatives of the conjugates include any salts, esters or derivatives that may be readily prepared by those of skill in this art using known methods for such derivatization and that produce compounds that may be administered
5 to animals or humans without substantial toxic effects and that either are pharmaceutically active or are prodrugs. A prodrug is a compound that, upon *in vivo* administration, is metabolized or otherwise converted to the biologically, pharmaceutically or therapeutically active form of the compound. To produce a prodrug, the pharmaceutically active compound is modified such that the active
10 compound will be regenerated by metabolic processes. The prodrug may be designed to alter the metabolic stability or the transport characteristics of a drug, to mask side effects or toxicity, to improve the flavor of a drug or to alter other characteristics or properties of a drug. By virtue of knowledge of pharmacodynamic processes and drug metabolism *in vivo*, those of skill in this art, once a pharmaceutically active compound
15 is known, can design prodrugs of the compound (*see, e.g.,* Nogrady (1985) *Medicinal Chemistry A Biochemical Approach*, Oxford University Press, New York, pages 388-392). In addition, the conjugates may be formulated as the sole pharmaceutically active ingredient in the composition or may be combined with other active ingredients.

The conjugates can be administered by any appropriate route, for
20 example, orally, parenterally, intravenously, intradermally, subcutaneously, or topically, in liquid, semi-liquid or solid form and are formulated in a manner suitable for each route of administration. Preferred modes of administration depend upon the indication treated. Dermatological and ophthalmologic indications will typically be treated locally; whereas, tumors and vascular proliferative disorders, will typically be
25 treated by systemic, intradermal, intralesional, or intramuscular modes of administration.

The conjugate is included in the pharmaceutically acceptable carrier in an amount sufficient to exert a therapeutically useful effect in the absence of undesirable side effects on the patient treated. It is understood that number and degree
30 of side effects depends upon the condition for which the conjugates are administered. For example, certain toxic and undesirable side effects are tolerated when treating life-threatening illnesses, such as tumors, that would not be tolerated when treating disorders of lesser consequence.

The concentration of conjugate in the composition will depend on
35 absorption, inactivation and excretion rates thereof, the dosage schedule, and amount administered as well as other factors known to those of skill in the art.

As used herein an effective amount of a compound for treating a particular disease is an amount that is sufficient to ameliorate, or in some manner reduce the symptoms associated with the disease. Such amount may be administered as a single dosage or may be administered according to a regimen, whereby it is effective.

- 5 The amount may cure the disease but, typically, is administered in order to ameliorate the symptoms of the disease. Repeated administration may be required to achieve the desired amelioration of symptoms.

- Typically a therapeutically effective dosage should produce a serum concentration of active ingredient of from about 0.1 ng/ml to about 50-100 µg/ml. The pharmaceutical compositions typically should provide a dosage of from about 0.01 mg to about 100 - 2000 mg of conjugate, depending upon the conjugate selected, per kilogram of body weight per day. Typically, for intravenous or systemic treatment a daily dosage of about between 0.05 and 0.5 mg/kg should be sufficient. Local application for ophthalmic disorders should provide about 1 ng up to 100 µg, preferably about 1 µg to about 10 µg, per single dosage administration. It is understood that the amount to administer will be a function of the conjugate selected, the indication treated, and possibly the side effects that will be tolerated. Dosages can be empirically determined using recognized models for each disorder.

- The active ingredient may be administered at once, or may be divided into a number of smaller doses to be administered at intervals of time. It is understood that the precise dosage and duration of treatment is a function of the disease being treated and may be determined empirically using known testing protocols or by extrapolation from *in vivo* or *in vitro* test data. It is to be noted that concentrations and dosage values may also vary with the severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of the compositions, and that the concentration ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed compositions.

- Solutions or suspensions used for parenteral, intradermal, subcutaneous, or topical application can include any of the following components: a sterile diluent, such as water for injection, saline solution, fixed oil, polyethylene glycol, glycerine, propylene glycol or other synthetic solvent; antimicrobial agents, such as benzyl alcohol and methyl parabens; antioxidants, such as ascorbic acid and sodium bisulfite; chelating agents, such as ethylenediaminetetraacetic acid (EDTA); buffers, such as acetates, citrates and phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose. Parental preparations can be enclosed in ampules.

disposable syringes or multiple dose vials made of glass, plastic or other suitable material. If administered intravenously, suitable carriers include physiological saline or phosphate buffered saline (PBS), and solutions containing thickening and solubilizing agents, such as glucose, polyethylene glycol, and polypropylene glycol and mixtures thereof. Liposomal suspensions may also be suitable as pharmaceutically acceptable carriers. These may be prepared according to methods known to those skilled in the art.

The conjugates may be prepared with carriers that protect them against rapid elimination from the body, such as time release formulations or coatings. Such carriers include controlled release formulations, such as, but not limited to, implants and microencapsulated delivery systems, and biodegradable, biocompatible polymers, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, polyorthoesters, polylactic acid and others. These are particularly useful for application to the eye for ophthalmic indications following or during surgery in which only a single administration is possible. Methods for preparation of such formulations are known to those skilled in the art.

The conjugates may be formulated for local or topical application, such as for topical application to the skin and mucous membranes, such as in the eye, in the form of gels, creams, and lotions and for application to the eye or for intracisternal or intraspinal application. Such solutions, particularly those intended for ophthalmic use, may be formulated as 0.01% -10% isotonic solutions, pH about 5-7, with appropriate salts. The ophthalmic compositions may also include additional components, such as hyaluronic acid. The conjugates may be formulated as aerosols for topical application (see, e.g., U.S. Patent Nos. 4,044,126, 4,414,209, and 4,364,923).

If oral administration is desired, the conjugate should be provided in a composition that protects it from the acidic environment of the stomach. For example, the composition can be formulated in an enteric coating that maintains its integrity in the stomach and releases the active compound in the intestine. The composition may also be formulated in combination with an antacid or other such ingredient.

Oral compositions will generally include an inert diluent or an edible carrier and may be compressed into tablets or enclosed in gelatin capsules. For the purpose of oral therapeutic administration, the active compound or compounds can be incorporated with excipients and used in the form of tablets, capsules or troches. Pharmaceutically compatible binding agents and adjuvant materials can be included as part of the composition. When the dosage unit form is a capsule, it can contain, in addition to material of the above type, a liquid carrier such as a fatty oil. In addition, dosage unit forms can contain various other materials which modify the physical form of the dosage unit, for example, coatings of sugar and other enteric agents. The

conjugates can also be administered as a component of an elixir, suspension, syrup, wafer, chewing gum or the like. A syrup may contain, in addition to the active compounds, sucrose as a sweetening agent and certain preservatives, dyes and colorings and flavors.

- 5 The active materials can also be mixed with other active materials that do not impair the desired action, or with materials that supplement the desired action, such as cis-platin for treatment of tumors.

- 10 Finally, the compounds may be packaged as articles of manufacture containing packaging material, one or more conjugates or compositions as provided herein within the packaging material, and a label that indicates the indication for which the conjugate is provided.

H. Therapeutic use of the VEGF conjugates

- 15 The conjugates provided herein can be used in pharmaceutical compositions to treat VEGF-mediated pathophysiological conditions by targeting to cells that bear VEGF receptors and inhibiting proliferation of or causing death of the cells. Such pathophysiological conditions include, for example, certain tumors, such as Kaposi's sarcoma, renal cell carcinomas and highly vascularized tumors, rheumatoid arthritis, psoriasis and other hyperproliferative skin disorders. As used herein, a
- 20 hyperproliferative skin disorder is a disorder that is manifested by a proliferation of endothelial cells of the skin coupled with an underlying vascular proliferation, resulting in a localized patch of scaly, horny or thickened skin or a tumor of endothelial origin. Such disorders include, but are not limited to actinic and atopic dermatitis, toxic eczema, allergic eczema, psoriasis, skin cancers and other tumors, such as Kaposi's
- 25 sarcoma, angiosarcoma, hemangiomas, and other highly vascularized tumors, and vascular proliferative responses, such as varicose veins. The treatment is effected by administering a therapeutically effective amount of the VEGF conjugate, for example, in a physiologically vehicle suitable for local or systemic application. In particular, for treatment of localized skin disorders the conjugate is formulated for topical, local or
- 30 intralesional application to the skin and is applied topically, locally or intralesional.

- 35 Treatment means any manner in which the symptoms of a conditions, disorder or disease are ameliorated or otherwise beneficially altered. Treatment also encompasses any pharmaceutical use of the compositions herein. Symptoms of a particular disorder are ameliorated by administration of a particular pharmaceutical composition and refers to any lessening, whether permanent or temporary, lasting or transient that can be attributed to or associated with administration of the composition.

The following examples are included for illustrative purposes only and are not intended to limit the scope of the invention.

5

EXAMPLE 1

RECOMBINANT PRODUCTION OF SAPORIN

A. Materials and methods

1. Bacterial Strains

10 *E. coli* strain JA221 (lpp⁻ hdsM⁺ trpE5 leuB6 lacY recA1 F'[lacI^s lac⁺ pro⁺]) is publicly available from the American Type Culture Collection (ATCC), Rockville, MD 20852, under the accession number ATCC 33875. (JA221 is also available from the Northern Regional Research Center (NRRL), Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604, under the accession number
15 NRRL B-15211; *see, also*, U.S. Patent No. 4,757,013 to Inouye; and Nakamura et al., *Cell* 18:1109-1117, 1979). Strain INV1 α is commercially available from Invitrogen, San Diego, CA.

2. DNA Manipulations

20 The restriction and modification enzymes employed herein are commercially available in the U.S. Native saporin and rabbit polyclonal antiserum to saporin were obtained as previously described in Lappi et al., *Biochem. Biophys. Res. Comm.* 129:934-942. Ricin A chain is commercially available from Sigma, Milwaukee, WI. Antiserum was linked to Affi-gel 10 (Bio-Rad, Emeryville, CA)
25 according to the manufacturer's instructions. Sequencing was performed using the Sequenase kit of United States Biochemical Corporation (version 2.0) according to the manufacturer's instructions. Miniprep and maxiprep of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media, Western blotting, and ELISA assays were according to Sambrook et al., (*Molecular*
30 *Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). The purification of DNA fragments was done using the GeneClean II kit (Bio 101) according to the manufacturer's instructions. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Western blotting was accomplished by transfer of the electrophoresed
35 protein to nitrocellulose using the PhastTransfer system, as described by the manufacturer. The antiserum to SAP was used at a dilution of 1:1000. Horseradish peroxidase labeled anti-IgG was used as the second antibody (*see* Davis et al., *Basic*

Methods In Molecular Biology, New York, Elsevier Science Publishing Co., pp 1-338. 1986).

B. Isolation of DNA encoding saporin

5 1. Isolation of genomic DNA and preparation of polymerase chain reaction (PCR) primers

Saponaria officinalis leaf genomic DNA was prepared as described in Bianchi et al., *Plant Mol. Biol.* 11:203-214, 1988. Primers for genomic DNA amplifications were synthesized in a 380B automatic DNA synthesizer. The primer
10 corresponding to the "sense" strand of saporin (SEQ ID NO. 1) includes an *EcoR* I restriction site adapter immediately upstream of the DNA codon for amino acid -15 of the native saporin N-terminal leader sequence (SEQ ID NO. 1):

5'-CTGCAGAATTCGCATGGATCCTGCTTCAAT-3'.

The primer 5'-CTGCAGAATTCGCCTCGTTTGACTACTTTG-3' (SEQ
15 ID NO. 2) corresponds to the "antisense" strand of saporin and complements the coding sequence of saporin starting from the last 5 nucleotides of the DNA encoding the carboxyl end of the mature peptide. Use of this primer introduced a translation stop codon and an *EcoRI* restriction site after the sequence encoding mature saporin.

20 2. Amplification of DNA encoding saporin

Unfractionated *Saponaria officinalis* leaf genomic DNA (1 µl) was mixed in a final volume of 100 µl containing 10 mM Tris-HCl (pH 8.3), 50 mM KCl, 0.01% gelatin, 2 mM MgCl₂, 0.2 mM dNTPs, 0.8 µg of each primer. Next, 2.5 U TaqI DNA polymerase (Perkin Elmer Cetus) was added and the mixture was overlaid with
25 30 µl of mineral oil (Sigma). Incubations were done in a DNA Thermal Cycler (Ericomp). One cycle included a denaturation step (94°C for 1 min.), an annealing step (60°C for 2 min.), and an elongation step (72°C for 3 min.). After 30 cycles, a 10 µl aliquot of each reaction was run on a 1.5% agarose gel to verify the correct structure of the amplified product.

30 The amplified DNA was digested with *EcoRI* and subcloned into *EcoR* I-restricted M13mp18 (see, Yanisch-Perron et al. (1985). *Gene* 33:103). Single-stranded DNA from recombinant phages was sequenced using oligonucleotides based on internal points in the coding sequence of saporin (see, Bennati et al., *Eur. J. Biochem.* 183:465-470, 1989). Nine of the M13mp18 derivatives were sequenced and
35 compared. Of the nine sequenced clones, five had unique sequences, set forth as SEQ ID NOS. 3-7, respectively. The clones were designated M13mp18-G4, -G1, -G2, -G7.

and -G9. Each of these clones contains all of the saporin coding sequence and 45 nucleotides of DNA encoding the native saporin N-terminal leader peptide.

C. pOMPAG4 Plasmid Construction

5 M13 mp18-G4, containing the SEQ ID NO. 3 clone from Example 1.B.2., was digested with *EcoR* I, and the resulting fragment was ligated into the *EcoR* I site of the vector pIN-IIIompA2 (*see, e.g., see*, U.S. Patent No. 4,575,013 to Inouye; and Duffaud et al., *Meth. Enz.* 153:492-507, 1987) using the methods described in Example 1.A.2. The ligation was accomplished such that the DNA encoding saporin,
10 including the N-terminal extension, was fused to the leader peptide segment of the bacterial ompA gene. The resulting plasmid pOMPAG4 contains the lpp promoter (Nakamura et al., *Cell* 18:1109-1117, 1987), the *E. coli* lac promoter operator sequence (lac O) and the *E. coli* ompA gene secretion signal in operative association with each other and with the saporin and native N-terminal leader-encoding DNA listed in SEQ
15 ID NO. 3. The plasmid also includes the *E. coli* lac repressor gene (lac I).

The M13 mp18-G1, -G2, -G7, and -G9 clones obtained from Example 1.B.2, containing SEQ ID NOS. 4-7 respectively, are digested with *EcoR* I and ligated into *EcoR* I digested pIN-IIIompA2 as described for M13 mp18-G4 above in this example. The resulting plasmids, labeled pOMPAG1, pOMPAG2, pOMPAG7,
20 pOMPA9, are screened, expressed, purified, and characterized as described for the plasmid pOMPAG4.

INV1 α competent cells were transformed with pOMPAG4 and cultures containing the desired plasmid structure were grown further in order to obtain a large preparation of isolated pOMPAG4 plasmid using methods described in Example 1.A.2.

25

D. Saporin expression in *E. coli*

The pOMPAG4 transformed *E. coli* cells were grown under conditions in which the expression of the saporin-containing protein is repressed by the lac repressor until the end of log phase of growth after which IPTG was added to induce
30 expression of the saporin-encoding DNA.

To generate a large-batch culture of pOMPAG4 transformed *E. coli* cells, an overnight culture (lasting approximately 16 hours) of JA221 *E. coli* cells transformed with the plasmid pOMPAG4 in LB broth (*see e.g.,* Sambrook et al., *supra*) containing 125 mg/ml ampicillin was diluted 1:100 into a flask containing 750 ml LB
35 broth with 125 mg/ml ampicillin. Cells were grown at logarithmic phase shaking at 37° C until the optical density at 550 nm reached 0.9 measured in a spectrophotometer.

In the second step, saporin expression was induced by the addition of IPTG (Sigma) to a final concentration of 0.2 mM. Induced cultures were grown for 2 additional hours and then harvested by centrifugation (25 min., 6500 x g). The cell pellet was resuspended in ice cold 1.0 M TRIS, pH 9.0, 2 mM EDTA (10 ml were added to each gram of pellet). The resuspended material was kept on ice for 20-60 minutes and then centrifuged (20 min., 6500 x g) to separate the periplasmic fraction of *E. coli*, which corresponds to the supernatant, from the intracellular fraction corresponding to the pellet.

10 E. Purification of secreted recombinant saporin

1. Anti-SAP immuno-affinity purification

The periplasmic fraction from Example 1.D. was dialyzed against borate-buffered saline (BBS: 5 mM boric acid, 1.25 mM borax, 145 mM sodium chloride, pH 8.5). The dialysate was loaded onto an immunoaffinity column (0.5 x 2 cm) of anti-saporin antibodies, obtained as described in Lappi et al., *Biochem. Biophys. Res. Comm.*, 129:934-942, 1985, bound to Affi-gel 10 and equilibrated in BBS at a flow rate of about 0.5 ml/min. The column was washed with BBS until the absorbance at 280 nm of the flow-through was reduced to baseline. Next the column containing the antibody bound saporin was eluted with 1.0 M acetic acid and 0.5 ml fractions were collected in tubes containing 0.3 ml of 2 M ammonium hydroxide, pH 10. The fractions were analyzed by ELISA (see, e.g., Sambrook et al., supra). The peak fraction of the ELISA was analyzed by Western blotting as described in Example 1.A.2 and showed a single band with a slightly higher molecular weight than native saporin. The fractions that contained saporin protein, as determined by the ELISA, were then pooled for further purification.

2. Reverse phase high performance liquid chromatography purification

To further purify the saporin secreted into the periplasm, the pooled fractions from Example 1.E.1. were diluted 1:1 with 0.1% trifluoroacetic acid (TFA) in water and chromatographed in reverse phase high pressure liquid chromatography (HPLC) on a Vydac C4 column (Western Analytical) equilibrated in 20% acetonitrile, 0.1% TFA in water. The protein was eluted with a 20 minute gradient to 60% acetonitrile. The HPLC produced a single peak that was the only area of immunoreactivity with anti-SAP antiserum when analyzed by a western blot as described in Example 1.E.1. Samples were assayed by an ELISA.

Sequence analysis was performed by Edman degradation in a gas-phase sequenator (Applied Biosystems) (*see, e.g., Lappi et al., Biochem. Biophys. Res. Comm.* 129:934-942, 1985). The results indicated that five polypeptides were obtained that differ in the length, between 7 and 12 amino acids, of the N-terminal saporin leader before the initial amino acid valine of the mature native saporin (SEQ ID NO.3: residue -12 through -7). All of the N-terminal extended variants retained cytotoxic activity. The size of the native leader is 18 residues, indicating that the native signal peptide is not properly processed by bacterial processing enzymes. The ompA signal was, however, properly processed.

To obtain homogeneous saporin, the recombinantly produced saporin can be separated by size.

F. Purification of intracellular soluble saporin

To purify the cytosolic soluble saporin protein, the pellet from the intracellular fraction of Example 1.E. above was resuspended in lysis buffer (30 mM TRIS, 2 mM EDTA, 0.1% Triton X-100, pH 8.0, with 1 mM PMSF, 10 µg/ml pepstatin A, 10 µg aprotinin, 10 µg/ml leupeptin and 100 µg/ml lysozyme, 3.5 ml per gram of original pellet). To lyse the cells, the suspension was left at room temperature for one hour, then frozen in liquid nitrogen and thawed in a 37°C bath three times, and then sonicated for two minutes. The lysate was centrifuged at 11,500 x g for 30 min. The supernatant was removed and stored. The pellet was resuspended in an equal volume of lysis buffer, centrifuged as before, and this second supernatant was combined with the first. The pooled supernatants were dialyzed versus BBS and chromatographed over the immunoaffinity column as described in Example 1.E.1. This material also retained cytotoxic activity.

G. Assay for cytotoxic activity

The RIP activity of recombinant saporin was compared to the RIP activity of native SAP in an *in vitro* assay measuring cell-free protein synthesis in a nuclease-treated rabbit reticulocyte lysate (Promega). Samples of immunoaffinity-purified saporin, obtained in Example 1.E.1., were diluted in PBS and 5 µl of sample was added on ice to 35 µl of rabbit reticulocyte lysate and 10 µl of a reaction mixture containing 0.5 µl of Brome Mosaic Virus RNA, 1 mM amino acid mixture minus leucine, 5 µCi of tritiated leucine and 3 µl of water. Assay tubes were incubated 1 hour in a 30°C water bath. The reaction was stopped by transferring the tubes to ice and adding 5 µl of the assay mixture, in triplicate, to 75 µl of 1 N sodium hydroxide, 2.5% hydrogen peroxide in the wells of a Millititer HA 96-well filtration plate (Millipore).

When the red color had bleached from the samples, 300 μ l of ice cold 25% trichloroacetic acid (TCA) were added to each well and the plate left on ice for another 30 min. Vacuum filtration was performed with a Millipore vacuum holder. The wells were washed three times with 300 μ l of ice cold 8% TCA. After drying, the filter paper
5 circles were punched out of the 96-well plate and counted by liquid scintillation techniques.

The IC_{50} for the recombinant and native saporin were approximately 20 pM. Therefore, recombinant saporin-containing protein has full protein synthesis inhibition activity when compared to native saporin.
10

EXAMPLE 2

RECOMBINANT PRODUCTION OF FGF-SAP FUSION PROTEIN

15 A. General Descriptions

1. Bacterial Strains and Plasmids:

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS were purchased from Novagen, Madison, WI. Plasmid pFC80, described below, has been described in the PCT Application No. WO 90/02800, except
20 that the bFGF coding sequence in the plasmid designated pFC80 herein has the sequence set forth as SEQ ID NO. 12, nucleotides 1-465. The plasmids described herein may be prepared using pFC80 as a starting material or, alternatively, by starting with a fragment containing the cII ribosome binding site (SEQ ID NO. 15) linked to the FGF-encoding DNA (SEQ ID NO. 12).

25 *E. coli* strain JA221 (lpp⁻ hdsM⁺ trpE5 leuB6 lacY recA1 F'[lacI^q lac⁺ pro⁺]) is publicly available from the American Type Culture Collection (ATCC), Rockville, MD 20852, under the accession number ATCC 33875. (JA221 is also available from the Northern Regional Research Center (NRRL), Agricultural Research Service, U.S. Department of Agriculture, Peoria, IL 61604, under the accession number
30 NRRL B-15211; *see, also*, U.S. Patent No. 4,757,013 to Inouye; and Nakamura et al., *Cell* 18:1109-1117, 1979). Strain INV1 α is commercially available from Invitrogen, San Diego, CA.

2. DNA Manipulations

35 Native SAP, chemically conjugated bFGF-SAP and rabbit polyclonal antiserum to SAP and FGF were obtained as described in Lappi et al., *Biochem. Biophys. Res. Comm.* 129:934-942, 1985, and Lappi et al., *Biochem. Biophys., Res. Comm.* 160:917-923, 1989. The pET System Induction Control was purchased from

Novagen, Madison, WI. The sequencing of the different constructions was done using the Sequenase kit of United States Biochemical Corporation (version 2.0). Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (*see, e.g., Sambrook et al., supra*). The purification of DNA fragments was done using the GeneClean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Rabbit polyclonal antiserum to SAP and FGF were obtained as described in Lappi et al., *Biochem. Biophys. Res. Comm.* 129:934-942, 1985, and Lappi et al., *Biochem. Biophys., Res. Comm.* 160:917-923, 1989. The pET System Induction Control was purchased from Novagen, Madison, WI. Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (*see, e.g., Sambrook et al., supra*). The purification of DNA fragments was done using the GeneClean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

Western blotting was accomplished by transfer of the electrophoresed protein to nitrocellulose using the PhastTransfer system, as described by the manufacturer. Horseradish peroxidase labeled anti-IgG was used as the second antibody (*see Davis et al., Basic Methods In Molecular Biology*, New York, Elsevier Science Publishing Co., pp. 1-338, 1986).

B. Construction of plasmids encoding FGF-SAP fusion proteins

1. Construction of FGFM13 that contains DNA encoding the CI ribosome binding site linked to FGF

A *Nco*I restriction site was introduced into the SAP-encoding DNA the M13mp18-G4 clone, prepared as described in Example 1.B.2. by site-directed mutagenesis method using the Amersham *in vitro*-mutagenesis system 2.1. The oligonucleotide employed to create the *Nco* I restriction site was synthesized using a 380B automatic DNA synthesizer (Applied Biosystems) and is listed as:

SEQ ID NO. 8 - CAACAACTGCCATGGTCACATC.

This oligonucleotide containing the *Nco* I site replaced the original SAP-containing coding sequence at SEQ ID NO.3, nts 32-53. The resulting M13mp18-G4 derivative is termed mpNG4.

In order to produce a bFGF coding sequence in which the stop codon was removed, the FGF-encoding DNA was subcloned into a M13 phage and subjected to site-directed mutagenesis. Plasmid pFC80 is a derivative of pDS20 (*see, e.g.,*

Duester et al., *Cell* 30:855-864, 1982; see, also, U.S. Patent Nos. 4,914,027, 5,037,74, 5,100,784, and 5,187,261; see, also, PCT Application No. WO 90/02800; and European Patent Application No. EP 267703 A1), which is almost the same as plasmid pKG1800 (see, Bernardi et al., *DNA Sequence* 1:147-150, 1990; see, also, McKenney et al. (1991) pp. 383-415 in *Gene Amplification and Analysis 2: Analysis of Nucleic Acids by Enzymatic Methods*, Chirikjian et al. (eds.), North Holland Publishing Company, Amsterdam) except that it contains an extra 440 bp at the distal end of *galK* between nucleotides 2440 and 2880 in pDS20. Plasmid pKG1800 includes the 2880 bp *EcoRI*-*Pvu* II of pBR322 that contains the contains the ampicillin resistance gene and an origin of replication.

Plasmid pFC80 was prepared from pDS20 by replacing the entire *galK* gene with the FGF-encoding DNA of SEQ ID NO. 12, inserting the *trp* promoter (SEQ ID NO. 14) and the bacteriophage lambda *cII* ribosome binding site (SEQ. ID No. 5; see, e.g., Schwarz et al., *Nature* 272:410, 1978) upstream of and operatively linked to the FGF-encoding DNA. The *trp* promoter can be obtained from plasmid pDR20 (Pharmacia PL Biochemicals) or synthesized according to SEQ ID NO. 14. Plasmid pFC80, contains the 2880 bp *EcoRI*-*Bam*HI fragment of plasmid pSD20, a synthetic *Sal* I-*Nde* I fragment that encodes the *Trp* promoter region (SEQ ID NO. 14):

EcoRI
 20 AATTCCCCTGTTGACAATTAATCATCGAACTAGTTAACTAGTACGCAGCTTGGCTGCAG
 and the *cII* ribosome binding site (SEQ ID NO. 15)):

Sal I *Nde* I
 GTCGACCAAGCTTGGGCATACATTCAATCAATTGTTATCTAAGGAAATACTTACATATG

The FGF-encoding DNA was removed from pFC80 by treating it as follows. The pFC80 plasmid was digested by *Hga* I and *Sal* I, which produces a fragment containing the *cII* ribosome binding site linked to the FGF-encoding DNA. The resulting fragment was blunt ended with *poll* (Klenow's fragment) and inserted into M13mp18 that had been opened by *Sma* I and treated with alkaline phosphatase for blunt-end ligation. In order to remove the stop codon, an insert in the ORI ~~min~~ direction was mutagenized, as described above, using the following oligonucleotide (SEQ ID NO. 9): GCTAAGAGCGCCATGGAGA. SEQ ID NO. 9 contains one nucleotide between the FGF carboxy terminal serine codon and a *Nco* I restriction site; it replaced the following wild type FGF encoding DNA having SEQ ID NO. 10:

35 GCT AAG AGC TGA CCA TGG AGA
 Ala Lys Ser STOP Pro Trp Arg

The resulting mutant derivative of M13mp18, lacking a native stop codon after the carboxy terminal serine codon of bFGF, was designated FGFM13. The mutagenized region of FGFM13 contained the correct sequence (SEQ ID NO. 11).

2. Preparation of plasmids pFS92 (PZ1A), PZ1B and PZ1C that encode the FGF-SAP fusion protein (FPFS1)

a. Plasmid pFS92 (also designated PZ1A)

5 Plasmid FGFM13 was cut with *Nco* I and *Sac* I to yield a fragment containing the cII ribosome binding site linked to the bFGF coding sequence with the stop codon replaced.

The M13mp18 derivative mpNG4 containing the saporin coding sequence was also cut with restriction endonucleases *Nco* I and *Sac* I, and the bFGF
10 coding fragment from FGFM13 was inserted by ligation to DNA encoding the fusion protein bFGF-SAP into the M13mp18 derivative to produce mpFGF-SAP, which contains the cII ribosome binding site linked to the FGF-SAP fusion gene. The sequence of the fusion gene is set forth in SEQ ID NO. 12 and indicates that the FGF protein carboxy terminus and the saporin protein amino terminus are separated by 6
15 nucleotides (SEQ ID NOS. 12 and 13, nts 466-471) that encode two amino acids Ala Met.

Plasmid mpFGF-SAP was digested with *Xba* I and *Eco*R I and the resulting fragment containing the bFGF-SAP coding sequence was isolated and ligated into plasmid pET-11a (available from Novagen, Madison, WI; for a description of the
20 plasmids see U.S. Patent No. 4,952,496; see, also, Studier et al., *Meth. Enz.* 185:60-89, 1990; Studier et al., *J. Mol. Biol.* 189:113-130, 1986; Rosenberg et al., *Gene* 56:125-135, 1987) that had also been treated with *Eco*R I and *Xba* I. The resulting plasmid was designated pFS92. It was renamed PZ1A.

Plasmid pFS92 (or PZ1A) contains DNA the entire basic FGF protein
25 (SEQ ID NO. 12), a 2-amino acid long connecting peptide, and amino acids 1 to 253 of the mature SAP protein. Plasmid pFS92 also includes the cII ribosome binding site linked to the FGF-SAP fusion protein and the T7 promoter region from pET-11a.

E. coli strain BL21(DE3)pLysS (Novagen, Madison WI) was transformed with pFS92 according to manufacturer's instructions and the methods
30 described in Example 2.A.2.

b. Plasmid PZ1B

Plasmid pFS92 was digested with *Eco*R I, the ends repaired by adding nucleoside triphosphates and Klenow DNA polymerase, and then digested with *Nde* I to release the FGF-encoding DNA without the cII ribosome binding site. This fragment
35 was ligated into pET 11a, which had been *Bam*H I digested, treated to repair the ends.

and digested with *Nde* I. The resulting plasmid was designated PZ1B. PZ1B includes the T7 transcription terminator and the pET-11a ribosome binding site.

E. coli strain BL21(DE3) (Novagen, Madison WI) was transformed with PZ1B according to manufacturer's instructions and the methods described in Example 2.A.2.

c. Plasmid PZ1C

Plasmid PZ1C was prepared from PZ1B by replacing the ampicillin resistance gene with a kanamycin resistance gene.

d. Plasmid PZ1D

Plasmid pFS92 was digested with *EcoR* I and *Nde* I to release the FGF-encoding DNA without the *cil* ribosome binding site and the ends were repaired. This fragment was ligated into pET 12a, which had been *Bam*H I digested and treated to repair the ends. The resulting plasmid was designated PZ1D. PZ1D includes DNA encoding the *ompT* secretion signal operatively linked to DNA encoding the fusion protein.

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS (Novagen, Madison WI) were transformed with PZ1D according to manufacturer's instructions and the methods described in Example 2.A.2.

EXAMPLE 3

PREPARATION OF MODIFIED SAPORIN

Saporin was modified by addition of a cysteine residue at the N-terminus-encoding portion of the DNA or by the addition of a cysteine at position 4 or 10. The resulting saporin is then reacted with an available cysteine on an FGF to produce conjugates that are linked via the added Cys or Met-Cys on saporin.

Modified SAP has been prepared by altering the DNA encoding the SAP by inserting DNA encoding Met-Cys at position -1 or by replacing the Ile or the Asp codon within 10 or fewer residues of the N-terminus with Cys. The resulting DNA has been inserted into pET 11a and pET 15b and expressed in BL21(DE3) cells. The resulting saporin proteins are designated FPS1 (saporin with Cys at -1), FPS2 (saporin with Cys at position 4) and FPS3 (saporin with Cys at position 10). A plasmid that encodes FPS1 and that has been used for expression of FPS1 has been designated PZ50B. Plasmids that encode FPS2 and that have been used for expression of FPS2 have been designated PZ51B (pET11a-based plasmid) and PZ51E (pET15b-based

plasmid). Plasmids that encode FPS3 and that have been used for expression of FPS3 have been designated PZ52B (pET11a-based plasmid) and PZ52E (pET 15b-based plasmid).

5 **A. Materials and Methods**

1. Bacterial strains

Novablue (Novagen, Madison, WI) and BL21(DE3) (Novagen, Madison WI).

10 **2. DNA manipulations**

DNA manipulations were performed as described in Examples 1 and 2. Plasmid PZ1B (designated PZ1B1 (the "1" at the end refers to the bacterial host strain, BL21(DE3)) described in Example 2 was used as the DNA template.

15 **B. Preparation of saporin with an added cysteine residue at the N-terminus**

The DNA encoding SAP-6 was amplified by polymerase chain reaction (PCR) from the parental plasmid pZ1B1 as described by McDonald et al. (1995). The plasmid pZ1B1 contains the DNA sequence for human FGF-2 linked to SAP-6 by a two amino acid linker (Ala-Met). pZ1B1 also includes the T7 promoter, lac operator, 20 ribosomal binding site, and T7 terminator present in the pET-11a vector. For SAP-6 DNA amplification, the 5' primer (5' CATATGTGTGTCACATCAATCAC ATTAGAT-3') (SEQ. ID No. 34) corresponding to the "sense" strand of SAP-6 incorporated a *NdeI* restriction enzyme site used for cloning. It also contained a Cys codon at position -1 relative to the start site of the mature protein sequence. No leader 25 sequence was included. The 3' primer (5' CAGGTTTGGATCCTTTACGTT 3') (SEQ. ID No. 35), corresponding to the "antisense" strand of SAP-6 has a *BamHI* site used for cloning. The amplified DNA was gel purified and digested with *NdeI* and *BamHI*. The digested SAP-6 DNA fragment was subcloned into the *NdeI* and *BamHI* digested pZ1B1. This digestion removed FGF-2 and the 5' portion of SAP-6 (up to nucleotide 30 position 650) from the parental rFGF2-SAP vector (pZ1B1) and replaced this portion with a SAP-6 molecule containing a Cys at position -1 relative to the start site of the native mature SAP-6 protein. The resultant plasmid was designated as pZ50B. pZ50B was transformed into *E. coli* strain NovaBlue for restriction and sequencing analysis. The appropriate clone was then transformed into *E. coli* strain BL21(DE3) for 35 expression and large scale production.

C. Preparation of saporin with a cysteine residue at position 4 or 10 of the native protein

These constructs were designed to introduce a cysteine residue at position 4 or 10 of the native protein by replacing the isoleucine residue at position 4 or the asparagine residue at position 10 with cysteine.

SAP was amplified by polymerase chain reaction (PCR) from the parental plasmid pZ1B encoding the FGF-SAP fusion protein using a primer corresponding to the sense strand of saporin, spanning nucleotides 466-501 of SEQ ID NO. 12, which incorporates a *NdeI* site and replaces the Ile codon with a Cys codon at position 4 of the mature protein (SEQ ID NO. 69):

CATATGGTCACATCATGTACATTAGATCTAGTAAAT.

or a primer corresponding to the sense strand of saporin, nucleotides 466-515 of SEQ ID NO. 12, incorporates a *NdeI* site and replaces the Asp codon with a Cys codon at position 10 of the mature protein (SEQ ID NO. 70)

CATATGGTCACATCAATCACATTAGATCTAGTATGTCCGACCGCGGGTCA.

The 3' primer complements the coding sequence of saporin spanning nucleotides 547-567 of SEQ ID NO. 12 and contains a *BamHI* site (SEQ ID NO. 35):

CAGGTTTGGATCCTTTACGTT.

The PCR amplification reactions were performed as described above, using the following cycles: denaturation step 94°C for 1 min, annealing for 2 min at 60°C, and extension for 2 min at 72°C for 35 cycles. The amplified DNA was gel purified, digested with *NdeI* and *BamHI*, and subcloned into *NdeI* and *BamHI* digested pZ1B. This digestion removed the FGF and 5' portion of SAP (up to the *BamHI* site) from the parental FGF-SAP vector (pZ1B) and replaced this portion with a SAP molecule containing a Cys at position 4 or 10 relative to the start site of the native mature SAP protein (see SEQ ID NOs. 29 and 30, respectively). The resulting plasmids are designated pZ51B and pZ52B, respectively.

D. Cloning of DNA encoding SAP mutants in vector pET15b

1. The SAP-Cys-1 mutants

The initial step in this construction was the mutagenesis of the internal *BamHI* site at nucleotides 555-560 (SEQ ID NO. 12) in pZ1B by PCR using a sense primer corresponding to nucleotides 543-570 (SEQ ID NO. 12) but changing the G at nucleotide 555 (the third position in the Lys codon) to an A. The complement of the sense primer was used as the antisense primer (SEQ ID NO. 73). The first round of amplification used primers SEQ ID NOs. 34 and 73 or 37 and 74 conducted as in B above. Individual fragments were gel purified and a second round of amplification was

performed using primers of SEQ ID Nos. 34 and 74 as in B, above. This amplification introduced a *NdeI* site and a Cys codon onto the 5' end of the saporin-encoding DNA. The antisense primer was complementary to the 3' end of the saporin protein and encoded a *BamHI* site for cloning and a stop codon (SEQ ID NO. 37):

5 GGATCCGCCTCGTTTGACTACTT.

The resulting fragment was digested with *NdeI/BamHI* and inserted into pET15b (Novagen, Madison, WI), which has a His-TagTM leader sequence (SEQ ID NO. 36), that had also been digested with *NdeI/BamHI*.

10 2. The SAP-Cys+4 and Sap-Cys+10 mutants

This construction was performed similarly to the SAP-Cys-1 using pZ1B as the starting material, and splice overlap extension (SOE) using PZ1B as the starting plasmid, including mutagenesis of the internal *BamHI* site at nucleotides 555-560 (SEQ ID NO. 12) in pZ1B by PCR using a sense primer corresponding to
15 nucleotides 543-570 (SEQ ID NO. 12) but changing the G at nucleotide 555 (the third position in the Lys codon) to an A and introduction of the cys at position 4 or 10 in place of the native amino acid.

The first round of amplification used primers of SEQ ID NOs. 69 and 73 (for the cys+4 saporin mutants) or SEQ ID NOs. 70 and 73 for the cys+10 saporin
20 mutants):

CATATGGTCACATCATGTACATTAGATCTAGTAAAT (SEQ ID NO. 69);

CATATGGTCACATCAATCACATTAGATCTAGTATGTCCGACCGCGGTCA (SEQ ID NO. 70);

TTTCAGGTTTGGATCTTTTACGTTGTTT (SEQ ID NO. 73).

Amplification conditions were as follows: denaturation for 1 min at
25 94°C, annealing for 2 min at 70°C and extension for 2 min at 72°C for 35 cycles. Individual fragments were gel purified and subjected to a second round of amplification, following the same protocol, using only the external oligos of SEQ ID NO. 37 and SEQ ID NO. 69 for the cys+4 mutant or SEQ ID NO. 70 for the cys+10 mutant. The resulting fragments had a *NdeI* site on the 5' end of the saporin-encoding
30 DNA and a *BamHI* site for cloning and a stop codon on the 3' end. The resulting fragment was digested with *NdeI/BamHI* and inserted into pET 15b (Novagen, Madison, WI), which has a His-TagTM leader sequence (SEQ ID NO. 36), that had also been digested *NdeI/BamHI*.

DNA encoding unmodified SAP (EXAMPLE 1) can be similarly
35 inserted into a pET15b or pET11a and expressed as described below for the modified SAP-encoding DNA.

E. Expression of the modified saporin-encoding DNA

The *E. coli* cells containing Cys-1 SAP construct were grown in a high cell density fed-batch fermentation with the temperature and pH controlled at 30°C and 6.9, respectively. A glycerol stock (1 mL) was grown in 50 ml of Luria Broth until
5 A_{600} reached 0.6. Inoculum (10 mL) was injected into a 7 L Applikon (Foster City, CA) fermentor containing 2 L of complex batch media consisting of 5 g/L of glucose, 1.25 g/L, each, of yeast extract and tryptone (Difco Laboratories, Detroit, MI, U.S.A.), 7 g/L of K_2HPO_4 , 8 g/L of KH_2PO_4 , 1.66 g/L of $(NH_4)_2SO_4$, 1 g/L of $MgSO_4 \cdot 7H_2O$, 2 mL/L of a trace metal solution (74 g/L of $Na_3Citrate$, 27 g/L of $FeCl_3 \cdot 6H_2O$, 2.0 g/L of $CoCl_2 \cdot 6H_2O$, 2.0 g/L of $Na_2MoO_4 \cdot 2H_2O$, 1.9 g/L of $CuSO_4 \cdot 5H_2O$, 1.6 g/L of $MnCl_2 \cdot 4H_2O$, 1.4 g/L of $ZnCl_2 \cdot 4H_2O$, 1.0 g/L of $CaCl_2 \cdot 2H_2O$, 0.5 g/L of H_3BO_3),
10 2 mL/L of a vitamin solution (6 g/L thiamine·HCl, 3.05 g/L of niacin, 2.7 g/L of pantothenic acid, 0.7 g/L of pyridoxine·HCl, 0.21 g/L of riboflavin, 0.03 g/L of biotin, 0.02 g/L of folic acid), and 100 mg/L of carbenicillin. The culture was grown for
15 12 hour before initiating the continuous addition of a 40x solution of complex batch media lacking the phosphates and containing only 25 mL/L, each, of trace metal and vitamin solutions. The feed addition continued until the A_{600} of the culture reached 85, at which time (approximately 9 h) the culture was induced with 0.1 mM IPTG. During 4 h of post-induction incubation, the culture was fed with a solution containing 100 g/L
20 of glucose, 100 g/L of yeast extract, and 200 g/L of tryptone. Finally, the cells were harvested by centrifugation (8,000 x g, 10 min) and frozen at -80°C until further processed.

F. Purification and conjugation of modified saporin

25 The cell pellet (~400 g wet weight) containing Cys-1 SAP was resuspended in 3 volumes of buffer B (10 mM sodium phosphate, pH 7.0, 5 mM EGTA, and 1 mM DTT). The suspension was passed through a microfluidizer three times at 18,000 lb/in² on ice. The resultant lysate was diluted with NanoPure H₂O until conductivity fell below 2.7 mS/cm. All subsequent procedures were performed at room
30 temperature.

The dilute lysate was loaded onto an expanded bed of Streamline SP cation-exchange resin (300 ml) pre-equilibrated with buffer C (20 mM sodium phosphate, pH 7.0, 1 mM EDTA) at 100 mL/min upwards flow. The resin was washed with buffer C until it appeared clear. The plunger was then lowered at 2 cm/min while
35 washing continued at 70 mL/min. Upwards flow was stopped when the plunger was approximately 8 cm away from the bed, and the plunger was allowed to move to within 0.5 cm of the packed bed. The resin was further washed at 70 mL/min downwards flow

until A_{280} reached baseline. Buffer C plus 0.25 M NaCl was then used to elute proteins containing Cys-1 SAP at the same flow rate.

The eluate was buffer exchanged into buffer D (50 mM sodium borate, pH 8.5, 1 mM EDTA) using the Sartocore Mini crossflow filtration system with a 10,000 NMWCO module (Sartorius, Goettingen, Germany). The sample was then applied to a column of Source 15S (30 mL) pre-equilibrated with buffer D. A 10 column volume linear gradient of 0 to 0.3 M NaCl in buffer D was used to elute Cys-1 SAP at 30 mL/min.

Both Cys-1 SAP and C96S FGF-2 were reduced with a final concentration of 10 mM DTT prior to gel filtration with buffer E (0.1 M sodium phosphate, pH 7.5, 0.1 M NaCl, 1 mM EDTA). The Cys-1 SAP was then reacted with 80-fold molar excess of DTNB at room temperature for 1 h, and the amount of Cys-1 SAP-TNB was determined by measuring absorbance at 412 nm using the molar absorption coefficient of $14,150 \text{ M}^{-1}\text{cm}^{-1}$. The Cys-1 SAP/DTNB mixture was subjected to size exclusion chromatography and eluted with buffer E. The C96S FGF-2 was added to the DTNB-treated Cys-1 SAP in a molar ratio of 3:1, and the reaction was carried out at 4°C overnight.

The reaction mixture was loaded onto a column of Heparin-Sepharose CL-4B pre-equilibrated with 0.5 M NaCl in buffer F (10 mM sodium phosphate, pH 6.0, 1 mM EDTA). The column was washed with 0.5 M then 1 M NaCl in buffer F, and the conjugate eluted with 2 M NaCl in buffer F. Fractions containing FGF2-Cys-1 SAP were combined, concentrated, and applied to a column of Superdex 75. Buffer G (10 mM sodium phosphate, pH 6.0, 0.15 M NaCl, 0.1 mM EDTA) was used for the Superdex 75 column.

During Cys-1 SAP purification, SDS-PAGE was performed on 12% acrylamide Mini-PROTEAN II Ready Gels (Bio-Rad, Hercules, CA, U.S.A.) according to the method of Laemmli (1970) under non-reducing conditions. PhastSystem using 10-15% acrylamide gradient gels.

30

EXAMPLE 4

PRODUCTION OF VEGF, VEGF-SAP AND SAP-VEGF CONSTRUCTS

A. General Descriptions

1. Bacterial Strains and Plasmids:

E. coli strains BL21(DE3), BL21(DE3)pLysS, HMS174(DE3) and HMS174(DE3)pLysS were purchased from Novagen. Madison, WI.

2. DNA Manipulations

Native SAP and rabbit polyclonal antiserum to SAP were obtained as described above or as described in Lappi et al. (1985) *Biochem. Biophys. Res. Comm.*, 129:934-942 and Lappi et al. (1989) *Biochem. Biophys. Res. Comm.*, 160:917-923. The pET System Induction Control was purchased from Novagen, Madison, WI. The sequencing of the different constructions was done using the Sequenase kit of United States Biochemical Corporation (version 2.0). Minipreparation and maxipreparations of plasmids, preparation of competent cells, transformation, M13 manipulation, bacterial media and Western blotting were performed using routine methods (see, e.g., Sambrook et al. (1989) *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY). The purification of DNA fragments was done using the Geneclean II kit, purchased from Bio 101. SDS gel electrophoresis was performed on a Phastsystem (Pharmacia).

3. Materials:

Bacterial strains: Novablue and BL21(DE3) (Novagen, Madison, WI).

Constructs that have been prepared include:

VEGF₁₆₅:SAP containing the VEGF leader sequence (amino acids 1-26; see, e.g., SEQ ID NO. 26);

VEGF₁₆₅:SAP without the leader sequence;

SAP:VEGF₁₆₅ containing the VEGF leader sequence;

SAP:VEGF₁₆₅ without the leader sequence;

VEGF₁₆₅ containing the leader sequence; and

VEGF₁₆₅ without the leader sequence; and similar constructs with VEGF₁₂₁ (see also Table 3).

Constructs containing any of VEGF₁₂₁, VEGF₁₈₉ and VEGF₂₀₆ in place of VEGF₁₆₅ are prepared in a similar manner except that DNA encoding VEGF₁₂₁ (SEQ ID NO. 25), VEGF₁₈₉ (SEQ ID NO. 27) and VEGF₂₀₆ (SEQ ID NO. 28) is used in place of the VEGF₁₆₅-encoding DNA in the above constructs, and, where necessary, appropriate amplification primers are selected.

VEGF-encoding DNA was obtained from plasmids designated pUC-121, pUC-165 and pUC-189 (the plasmids were the gift of Judith Abraham). Each of these plasmids had been prepared by inserting the respective DNA clone containing each form of VEGF linked to the signal peptide (see, SEQ ID NO. 26, nucleotides 13-90) into the *Bam*HI site of the well known and commercially available vector pUC18 (for descriptions of this vector, see, e.g., U.S. Patent Nos. 5,114,840, 4,992,051.

4,968,613, 4,898,828; see, also Yanisch-Perron et al. (1985) *Gene* 33:103-119; Norrander et al. (1983) *Gene* 26:101-106; available from, for example, Life Technologies, Inc, Rockville, MD).

5 **B. Construction of plasmids encoding VEGF-SAP fusion proteins**

1. Construction of plasmids that contains DNA encoding VEGF₁₆₅

a. Cloning

(i) VEGF₁₆₅-SAP constructs

The VEGF₁₆₅-SAP constructs were prepared using the parental
10 FGF:SAP vector pZ1B (pET 11a-based vector; see Example 2) that had been digested with *Nde*I and *Nco*I in order to remove the FGF-encoding portion of the DNA encoding the fusion protein, but leave the SAP-encoding portion intact. The FGF-encoding region was then replaced with the VEGF₁₆₅-encoding DNA that has a *Nde*I site at the 5' end and a *Nco*I site at the 3' end.

15

(ii) VEGF₁₆₅ constructs

To express the VEGF₁₆₅ protein without saporin, the pET11a vector was digested with *Nde*I and *Bam*HI and the VEGF sequence inserted with the appropriate ends. For the constructs containing VEGF alone, the 3' primer contained a
20 *Bam*HI site for cloning and encodes a stop codon as follows:

5' GGATCCTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 64).

b. Amplification

(i) VEGF₁₆₅-SAP constructs with the leader sequence

25 The constructs with the VEGF leader sequence were prepared from VEGF₁₆₅ as the template. For plasmids containing VEGF with the leader sequence or VEGF-SAP containing the leader sequence of the VEGF, the 5' primer contained a *Nde*I restriction enzyme site and encodes the signal sequence as follows:

5' CATATGAACTTTCTGCTGTCTTGG 3' (SEQ ID NO. 62), which
30 contains a *Nde*I restriction enzyme site and encodes the signal. The *Nco*I site within VEGF₁₆₅ was removed by SOE as the first step in the preparation of this construct using oligonucleotides of SEQ ID NOs. 60 and 61. The first round of PCR used oligos of SEQ ID NOs. 62 and 61 and SEQ ID NOs. 60 and 65.

5' TCCCAGGCTGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 60: sense
35 primer); 5' TCCTCCTTCTGCCATTGGTGCAGCCTGGGA 3' (SEQ ID NO. 61: the complement or "antisense" primer); and 5' CCATGGCCGCCTCGGCTTGTC 3' (SEQ ID NO. 65: 3' primer that removes the stop codons and introduces a *Nco*I site).

Amplification was performed as follows: denaturation for 1 min at 94°C annealing for 2 min at 70°C and extension for 2 min at 72°C for 35 cycles. Individual fragments were gel purified and subjected to a second round of amplification using only the external oligos (SEQ ID NOs. 62 and 65) under the same amplification conditions as above, to generate full length fragments which contain the appropriate cloning sites at the ends. After amplification and purification, the inserts are directionally cloned into the sites *NdeI*/*NcoI*-digested PZ1B.

(ii) **VEGF₁₆₅-SAP constructs without the leader sequence**

To prepare the constructs that lack DNA encoding the leader sequence, a similar amplification was performed with a primer similar to SEQ ID NO. 62, but lacking the signal sequence and beginning at position 1 of the mature protein as follows:

5' CATATGGCACCAATGGCAGAAGGAGGAGG 3'(SEQ ID NO. 63).

2. Construction of plasmids that contain DNA encoding VEGF₁₂₁

The same type of constructs are generated using DNA encoding the VEGF₁₂₁-encoding DNA, except that DNA encoding VEGF₁₂₁ (see, SEQ. ID NO. 25) is used in place of the DNA encoding VEGF₁₆₅. The initial step requires the mutagenesis of an internal *NcoI* site located at position 95 in the mature VEGF protein by nucleic acid amplification using the VEGF₁₂₁-encoding DNA as a source of DNA.

The "sense" oligo the primer has the sequence:

5' TCCCAGGCTGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 60);

and the complement or "antisense" primer has the sequence:

5' TCCTCCTTCTGCCATTGGTGCAGCCTGGGA 3' (SEQ ID NO. 61) as described for VEGF₁₆₅.

For the VEGF₁₂₁ or VEGF₁₂₁-SAP constructs that contain the leader sequence the 5' primer has the following sequence:

5' CATATGAACCTTCTGCTGTCTTGG 3' (SEQ ID NO. 62).

This primer contains a *NdeI* restriction enzyme site and encodes the signal sequence. A second amplification is performed with similar primer that lacks the signal sequence and begins at position 1 of the mature protein. This primer has the following sequence:

5' CATATGGCACCAATGGCAGAAGGAGGAGG 3' (SEQ ID NO. 63).

For the constructs containing VEGF alone, the 3' primer contains a *BamHI* site for cloning and encodes a stop codon. This primer has the following sequence:

5' GGATCCTCATCACCGCCTCGGCTT 3'(SEQ ID NO. 64).

For the constructs designed to express the VEGF-SAP fusion protein, the stop codons have been removed and a *NcoI* site is introduced onto the 3' primer that has the sequence:

5' CCATGGCCGCCTCGGCTTGTC 3' (SEQ ID NO. 65).

The amplification conditions followed the above protocol.

C. Construction of plasmids encoding SAP-VEGF fusion proteins

The following constructs have been prepared:

- 1) SAP-VEGF₁₂₁
- 2) SAP-VEGF₁₆₅
- 3) SAP-linker-VEGF₁₂₁
- 4) SAP-linker-VEGF₁₆₅
- 5) SAP-linker-VEGF₁₂₁-linker-VEGF₁₂₁
- 6) SAP-linker-VEGF₁₆₅-linker-VEGF₁₆₅

in which the linker is (Gly₄Ser)_n, where n is selected from 1, 2 or 4. DNA encoding any other suitable peptide linker, *see, e.g.*, SEQ ID NOs. 38-50, can be substituted for the exemplified linkers. For other constructs, see Table 3.

Constructs 1-4 serve as cloning intermediates for the final forms 5 and 6.

All forms have been completely characterized.

All cloning was performed using the vector pET-SAPMCS. The starting material for this vector can be PZIA or any of the pET 11a based vectors herein. Unmodified saporin can be cloned, using PCR amplification with appropriate primers, into the and *NcoI* sites of the pET11a-based vector. Using appropriate primers, an *EcoRI* site is added 5' to and adjacent to the *NdeI* site, and an *EcoRI* site is added 3' to and adjacent to the *NcoI* site. The resulting amplified fragment is digested with *EcoRI* and subcloned into the *EcoRI* site of plasmid pGEM-4 (pGEM-4 serves as the source of the MCS, the pGEM series of plasmids are available from Promega, Madison WI; see also, U.S. Patent No. 4,766,072, which describes construction of the pGEM plasmids) in an orientation. such that the multicloning site (MCS) of pGEM-4 is 3' of the saporin-encoding sequences. In such constructs, the resulting plasmid (pGEMSAP) was digested with *PstI* and the ends of the fragment were blunt-ended. The fragment was then digested with *NdeI*, thereby generating a fragment that contains all of the saporin-encoding DNA and most of the MCS of pGEM-4. This fragment was then cloned into the *NdeI/BamHI* sites of pET 11a, in which the *BamHI* site had been blunt-ended by filling in with Klenow polymerase and then cut with *NdeI* to produce *NdeI/BamHI* blunt ends. The resulting plasmid was designated PETSAP-MCS. It has unique *SacI*.

*Sma*I, and *Sal*I sites in the MCS for insertion of DNA encoding a desired linker, VEGF monomer, or combination of VEGF and linker 3' of the saporin-encoding DNA.

1. SAP-VEGF₁₂₁ and SAP-VEGF₁₆₅

5 The VEGF-encoding DNA is cloned downstream from SAP using the NcoI site at the C-terminus of SAP and one of several enzyme sites contained in the flanking region. For these constructs the VEGF molecule was amplified from cDNA using oligos that introduce a NcoI (CCATGG) site onto the N-terminus of the mature protein (and also remove an internal NcoI), and introduce a stop codon at the C-terminus of VEGF as well as a *Sal*I (GTCGAC) site for cloning. In each case, the appropriate parental vector was digested with NcoI and *Sal*I, and a NcoI/*Sal*I digested insert was cloned into that site. PCR conditions were as for the amplification reactions described above.

Amplification was done using the following 5' sense oligo:

15 5' CCATGGCACCAATGGCAGAAGGAGGA 3' (SEQ ID NO. 51),

and 3' anti-sense oligo:

5' GTCGACTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 52).

2. SAP-linker-VEGF₁₂₁ and SAP-linker-VEGF₁₆₅

20 For the generation of the linker-VEGF constructs, a different 5' primer that adds a NcoI site to the N-terminus, mutates the internal NcoI site and adds either the DNA encoding (Gly₄Ser) (SEQ ID NO. 40), designated X1, or (Gly₄Ser)₂ designated X2 (SEQ ID NO. 41) onto the N-terminus of the VEGF molecule was used. The 3' primer was the above oligonucleotide (SEQ ID NO. 52). For the constructs with the (Gly₄Ser)-encoding DNA, the 5' primer oligo was:

25 5' CCATGGGCGGCGGCGGCTCTGCACCAATGGCAGAAGGA 3' (SEQ ID NO. 53).

For the (Gly₂Ser)₂ linker, this oligo was:

30 5'CCATGGGCGGCGGCGGCTCTGGCGGCGGCGGCTCTGCACCAATGGCAGAA GGA 3'

(SEQ ID NO. 54). The sequence of SAP-(Gly₄Ser)- VEGF₁₂₁ is set forth in SEQ ID NO. 57. The sequence of SAP-(Gly₄Ser)-VEGF₁₆₅ is set forth in SEQ ID NO. 58.

The construct in which the linker is (Gly₄Ser)₄ was prepared by digesting a plasmid (designated PZ74B or PZ74F) which contains SAP-AlaMet-VEGF₁₆₅ construct with NcoI and inserting a fragment encoding NcoI- (Gly₄Ser)₄-NcoI (prepared, for example, by inserting codons encoding (Gly₄Ser)₂ between the Gly₄Ser and Gly₄Ser in SEQ ID NO. 41).

3. SAP-linker-VEGF₁₆₅-linker-VEGF₁₆₅ and SAP-linker-VEGF₁₂₁-linker-VEGF₁₂₁ constructs

For construction of the SAP-linker-VEGF-linker-VEGF constructs, the same 5'oligos were used for the constructs incorporating (Gly₄Ser)₁ and (Gly₄Ser)₂ (see, SEQ ID NOs. 53 and 54, respectively) and a set of 3' oligos were prepared that incorporated (Gly₄Ser)₁ or (Gly₄Ser)₂ and a NcoI site. The SAP-AlaMet-VEGF parental construct was digested with NcoI and the NcoI-linker-VEGF-NcoI fragment was inserted to produce constructs containing SAP-linker-VEGF-linker-VEGF.

The C-terminus oligos for the (Gly₄Ser)₁ linker was:
5'CCATGGCAGAGCCGCGCCGCCCCGCTCGGCTTGTCACAT 3' (SEQ ID NO. 55). The (Gly₄Ser)₂ linker for the 3' portion was (SEQ ID NO. 56):
5'CCATGGCAGAGCCGCGCCGCGCCAGAGCCGCGCCGCCCCGCTCGGCTTGTCACAT 3'. Amplification conditions were as described above.

The sequence of SAP-(Gly₄Ser)-VEGF₁₂₁-(Gly₄Ser)-VEGF₁₂₁ is set forth is SEQ ID NO. 78 and the sequence of SAP-(Gly₄Ser)-VEGF₁₆₅-(Gly₄Ser)-VEGF₁₆₅ is set forth in SEQ ID NO. 79.

4. SAP-Linker-VEGF₁₂₁ constructs

These constructs were prepared in a similar manner to the VEGF₁₆₅-containing constructs, except that plasmids containing VEGF₁₂₁ were used as the starting materials.

D. Expression of the SAP-VEGF and SAP-LINKER-VEGF constructs

The plasmids containing the various SAP-VEGF and SAP-LINKER-VEGF constructs (see Table 3) have been introduced into various vectors and host and are cultured under conditions suitable for expression in the selected host/vector. The resulting fusion protein is then purified as described for VEGF using heparin sulfate (see, e.g., U.S. Patent No. 5,219,739 to Tischer et al.; U.S. Patent No. 5,194,596 to Tisher et al.; U.S. Patent No. 5,240,848 to Keck et al.; International PCT Application No. WO 90/13649, which is based on U.S. applications serial nos. 07/351,361, 07/369,424, 07/389,722, to Genentech, Inc., and any U.S. Patent based U.S. applications Serial Nos. 07/351,361, 07/369,424, 07/389,722; European Patent Applications EP 0 506 477 A1 and EP 0 476 983 A1 to MERCK & CO.; Houck et al. (1991) *Mol. Endo.* 5:1806-1814). An affinity column with anti-SAP antibody may alternatively be used to purify VEGF conjugates, especially for SAP-VEGF₁₂₁.

E. Cytotoxicity of VEGF fusion protein conjugates

Cytotoxicity experiments are performed with the Promega (Madison, WI) CellTiter 96 Cell Proliferation/Cytotoxicity Assay. About 1,500 bovine or human aortic endothelial cells or other vascular endothelial cells are plated per well in a 96 well plate in 90 μ l HDMEM plus 10% FCS and incubated overnight at 37°C, 5% CO₂. The following morning 10 μ l of media alone or 10 μ l of media containing various concentrations of the fusion protein, VEGF dimer or saporin are added to the wells. The plate was incubated for 72⁰ C hours at 37 C. Following the incubation period, the number of living cells are determined by measuring the incorporation and conversion of the commonly available dye MTT supplied as a part of the Promega kit. Fifteen μ l of the MTT solution was added to each well, and incubation was continued for 4 hours. Next, 100 μ l of the standard solubilization solution supplied as a part of the Promega kit are added to each well. The plate is allowed to stand overnight at room temperature and the absorbance at 560 nm was read on an ELISA plate reader (Titertek Multiskan PLUS, ICN, Flow, Costa Mesa, CA).

EXAMPLE 5

BACULOVIRUS EXPRESSION OF VEGF

A. Materials:

The VEGF constructs, including the VEGF₁₂₁, VEGF₁₂₁:SAP, VEGF₁₆₅ and VEGF₁₆₅:SAP constructs containing the leader sequences are introduced into a baculovirus vector pBluebac III (Invitrogen, San Diego, CA) and then co-transfected with wild type virus into insect cells *Spodoptera frugiperda* (sf9; see, e.g., Luckow et al. (1988) *Bio/technology* 6:47-55 and U.S. Patent No. 4,745,051) cells).

Antisera to VEGF was obtained from R&D/Peprtech (polyclonal anti-native VEGF) and Santa Cruz (polyclonal anti-VEGF peptide antibody).

Constructs that are prepared include: VEGF₁₂₁ containing the leader sequence and VEGF₁₆₅ containing the leader sequence. The fusion proteins in which saporin is linked to the N-terminus of a VEGF monomer are presently preferred for baculovirus expression (and also bacterial expression). Heterologous leader sequences. discussed below, that direct secretion of the encoded fusion protein are added.

B. Amplification

The template for these constructs is the VEGF₁₂₁ or VEGF₁₆₅ or the VEGF₁₆₅:SAP construct containing the leader sequence in pET11a, described above. The 5' oligo (sense) for the VEGF₁₂₁, VEGF₁₂₁:SAP and VEGF₁₆₅ constructs contains a *Bam*HI I site for cloning into the vector and is as follows:

5' GGATCCGAAACATGAACTTTCTGCTGTCT 3' (SEQ ID NO. 66).

The VEGF₁₆₅:SAP construct is amplified from the existing VEGF₁₆₅:SAP insert in pET11a using the following 5' oligo, which contains a *Bam*HI I site for cloning and is:

10 5' GGATCCGAAACATATGAACTTTCTGCTGTCT 3' (SEQ ID NO. 67).

The 3' or non-coding oligo for the VEGF₁₂₁:SAP or VEGF₁₆₅:SAP constructs contains a *Pst*I I site for cloning into the vector and has the sequence:

5' CTGCAGGCCTCGTTTGACTACTT 3' (SEQ ID NO. 71).

The oligo for the 3' end of the VEGF₁₂₁ and VEGF₁₆₅ has the sequence (SEQ ID NO. 68): 3' CTGCAGTCATCACCGCCTCGGCTT 3'. Amplification follows the same protocol as described in the above Examples: denaturation for 1 min at 94°C, annealing for 2 min at 70°C, and extension for 2 min at 72°C for 35 cycles.

20 **C. Cloning**

The inserts are directionally cloned into the *Bam*HI/*Pst*I sites of pBlueBac III.

25 **D. Preparation of VEGF molecules with an accessible cysteine residue at the N-terminus for chemical conjugation**

VEGF molecules with an accessible cysteine residue at the N-terminus are constructed. These molecules can be chemically conjugated to one of the SAP muteins (Cys -1, +4 or +10 as described above). These constructs are as follows:

- 1) VEGF₁₂₁ with a cys at +4
- 2) VEGF₁₆₅ with a cys at +4
- 3) VEGF₁₂₁ with a cys at +2 followed by a *Nco*I site which makes this construct linker amenable.
- 4) VEGF₁₆₅ with a cys at +2 followed by a *Nco*I site for the linker amenable form.

35 These constructs are designed such that the distance between the molecules (or accessible cysteines) can be increased by adding various linkers encoded on a *Nco*I (CCATGG) fragment, and thereby decrease any steric hindrance. The

presently preferred linkers are the linkers set forth in $(\text{Gly}_4\text{Ser})_n$, in which $n=1-4$, linkers (see, SEQ ID NOs. 40 and 41, for $n=1$ and 2).

Amplification of the template for these constructs is VEGF₁₂₁ or VEGF₁₆₅-encoding DNA (see, SEQ ID NOs. 25 and 26, respectively). The 5' sense oligo for the introduction/insertion of the mutations into the mature forms of the proteins VEGF_{121/165} cys+4 constructs (1 and (2 above) is:

5' TGGTCCCAGGCTGCACCCATGTGTGAAGGAGGAGGGCAGAATCAT 3'
(SEQ ID NO. 80).

The corresponding anti-sense mutational oligo is:

10 5' ATGATTCTGCCCTCCTCCTTCACACATGGGTGCAGCCTGGGACCA 3'(SEQ ID NO. 81).

The 5' sense oligo for the introduction/insertion of the cys mutations into the mature forms of the proteins VEGF_{121/165} cys+2 NcoI constructs (3 and (4, above is:

15 5' GCCAAGTGGTCCCAGGCTGCATGTCCCATGGCAGAAGGAGGAGGGCAG 3'
(SEQ ID NO. 82).

The corresponding anti-sense mutational oligo is:

5' CTGCCCTCCTCCTTCTGCCATGGGACATGCAGCCTGGGACCACTTGGC 3'
(SEQ ID NO. 83).

20 The 5' sense oligo containing the *Bam*HI (GGATCC) cloning site for introduction into the baculovirus transfer vector pBlueBacIII for each of the above forms (1- (4, above, is:

5' GGATCCGAAACATGAACTTTCTGCTGTCT 3' (SEQ ID NO. 66).

The 3' anti-sense oligo containing the *Pst*I (CTGCAG) site for cloning into the pBlueBacIII transfer vector for each of the above constructs is:

25 5' CTGCAGTCATCACCGCCTCGGCTT 3' (SEQ ID NO. 68).

The constructs are prepared by splicing by overlap extension (SOE) by amplification of two pieces of the protein, which are then put together by the SOE technique. For example, to generate the VEGF cys+4 forms the first round of amplification uses oligos of SEQ ID NOs. 81 and 66 and SEQ ID NOs. 80 and 68. For the VEGF cys+2 NcoI constructs the first round of PCR would use oligos of SEQ ID NOs. 66 and 83 and 82 and 68. After amplification as follows: denaturation for 1 min at 94°C, annealing for 2 min at 70°C and extension for 2 min at 72°C. individual fragments are gel purified and subjected to a second round of amplification using only the external oligos (SEQ ID NOs. 66 and 68). under the same amplification conditions as above, to generate full length fragments which contain the appropriate cloning sites

at the ends. After amplification and purification, the inserts are directionally cloned into the *Bam*HI and *Pst*I sites of the pBlueBacIII transfer vector.

The constructs and corresponding Sequence Listing ID Nos. are as follows:

- 5 1) VEGF₁₂₁ cys +4 is set forth in SEQ ID NO. 86;
- 2) VEGF₁₆₅ cys +4 is set forth in SEQ ID NO. 87;
- 3) VEGF₁₂₁ Cys+2 with NcoI sites is set forth in SEQ ID NO. 88;
- and
- 4) VEGF₁₆₅ Cys+2 with NcoI is set forth in SEQ ID NO. 89.

10

E. Preparation of SAP:VEGF constructs with heterologous signal (leader) sequences

Constructs containing a heterologous signal sequence in place of the VEGF signal sequence (*see, e.g.*, amino acids 1-26 in SEQ ID NO. 33) or in addition to
15 it are prepared. Such constructs are prepared using vectors such as pPBac and pMBac (available from Stratagene, San Diego, CA, *see, also* Lernhardt et al. (1993) *Strategies* 6:20-21), which contain the human alkaline phosphatase (*see, e.g.*, Bailey et al. (1989) *Proc. Natl. Acad. Sci. U. S. A.* 86:22-26) and melittin (*see, e.g.*, Tessier et al. (1991) *Gene* 98:177-183) secretory signals inserted into the *Bam*HI and *Nde*I sites,
20 respectively of pJVP10Z (*see, e.g.*, Kawamoto et al. (1991) *Biochem. Biophys. Res. Commun.* 181:756-63, Ueda et al. (1994) *Gene* 140:267-272. Insertion of genes into the *Sma*I/*Bam*HI sites of these vectors results in fusion proteins that are directed into the insect cell secretory pathway, which processes the pro-polypeptide so that mature peptide or fusion protein is secreted into the growth medium.

25 Other heterologous signal sequences, such as the insulin signal sequence (*see, e.g.*, U.S. Patent No. 4,431,746 for DNA encoding the signal sequence), the growth hormone signal sequence, mammalian alkaline phosphatase, the mellitin signal sequence and others that are processed by insect cells are used.

The heterologous signal sequences are used in other constructs as well,
30 including VEGF:SAP constructs, in order to direct the proteins encoded by operatively linked DNA into the periplasmic space or growth medium.

F. Expression of the VEGF fusion protein-encoding constructs

The plasmids containing the various SAP-VEGF and SAP-linker-VEGF
35 constructs (see Table 3) have been introduced into the baculovirus host and are cultured under conditions suitable for expression in the selected host/vector. The resulting fusion proteins are then purified.

G. Characterization of the VEGF-SAP fusion protein**1. Western blot of affinity-purified VEGF-SAP fusion protein**

SDS gel electrophoresis was performed on a Phastsystem utilizing
5 10-15% gels (Pharmacia). Western blotting was accomplished by transfer of the
electrophoresed protein to nitrocellulose using the PhastTransfer system (Pharmacia),
as described by the manufacturer. The antisera to SAP and VEGF are used at a dilution
of 1:1000 dilution. Horseradish peroxidase labeled anti-IgG was used as the second
antibody (Davis et al. (1986) *Basic Methods in Molecular Biology*, New York, Elsevier
10 Science Publishing Co., pp 1-338).

2. Assays to assess the cytotoxicity of the VEGF-SAP fusion protein**a. Effect of VEGF-SAP fusion protein on cell-free protein
synthesis**

15 The RIP activity of VEGF fusion protein is assayed as described in
procedures for FGF conjugates (*see, e.g.*, U.S. Patent No. 5,191,067).

b. Cytotoxicity of VEGF-SAP fusion protein

Cytotoxicity of the VEGF fusion protein is assayed as described in U.S.
20 Patent No. 5,191,067), except that vascular endothelial cells, such as a human or bovine
aortic endothelial cells, are used. Prior to contacting with the VEGF conjugate the
VEGF receptors can be up-regulated. Briefly, the cells are seeded at density of $1 - 5 \times 10^4$
cells/per well (in 24 well plates) and are incubated with varying concentrations of
the test protein at 37°C for 5-7 days. Prior to contacting with the test protein the
25 VEGF receptors can be upregulated, such as by replating or pretreating with VEGF.
The cells are then trypsinized and counted in a Coulter counter.

EXAMPLE 6**30 EXPRESSION OF VEGF AND VEGF-SAP IN THE pP_L - λ SYSTEM**

The VEGF₁₂₁, VEGF₁₆₅, VEGF₁₂₁:SAP, VEGF₁₆₅:SAP,
SAP:VEGF₁₂₁, SAP:VEGF₁₆₅ constructs are also expressed in the pP_L - λ system
(Pharmacia Fine Chemicals, *see, also*, U.S. Patent No. 5,227,469). This system is
35 temperature inducible and directs the expressed protein to inclusion bodies thus
protecting the protein from degradation. The *EcoRI* and *XbaI* sites are used for
isolation of the VEGF or VEGF-SAP-encoding DNA from existing constructs.

Constructs are cloned into the unique *HpaI* site of pP_L-lambda (see, e.g., Remaut et al. (1981) *Gene* 15:81, available from Pharmacia). The P_L promoter, which is controlled by the cI repressor of λ , can be thermo-regulated using a bacterial host strain (N4830-1) containing the temperature-sensitive cI857 repressor. Induction is effected by raising the temperature.

All cloning is done in a host such as N99CI⁺ and then transferred into N4830-1 for induction. Thus, the plasmid containing the construct is introduced into the host and grown at 30°C until A600 = 0.8-1.0. The temperature is raised to 42°C for 2 hours and the expressed protein is targeted to inclusion bodies.

For example, a plasmid, such as PZ70B1, is digested with *XbaI*/*EcoRI* to release a fragment that contains the *XbaI*-ribosome binding site-VEGF₁₆₅-SAP-T7 terminator-*EcoRI* site, and the ends are filled in with Klenow reagent. Plasmid pP_L- λ is digested with *HpaI* and the blunt-ended fragment is ligated into the digested plasmid. The plasmid is introduced into the N4830-1, grown at 30°C and induced at 42°C. The fusion protein is recovered from the inclusion bodies.

The inclusion bodies are released from the cells by concentrating the cells, such as by centrifugation, and are resuspended in a buffer (~0.4-0.6 M salt). The cells are lysed, either mechanically by homogenization or enzymatically, such as by treatment with lysozyme or EDTA. Soluble materials are removed by sequential centrifugation and resuspension or diafiltration. Further purification can be effected by centrifugation in a sucrose gradient.

The purified inclusion body fraction is then solubilized and the residual insoluble material is pelleted and discarded. Solubilization is effected using either guanidine HCl 100mM, Tris, 150mM NaCl, 50mM EDTA and 50mM EGTA. Reducing agents, such as β -mercaptoethanol (0.1-0.3 M) and dithiothreitol (0.1 M) in the presence of EDTA are also used to disrupt disulfide bonds. The soluble protein fraction is recovered by centrifugation and diluted 10x into a buffer containing 100mM. This 10mM EDTA, 1% monothioglycerol and .25 M L-arginine, pH 9.5. The mixture is stored for 2 hours at 4°C and the centrifugation is repeated. Soluble protein is dialyzed in PBS to remove the monothioglycerol.

An acid phosphatase based assay is used to determine the level of proliferation induced by the addition of VEGF to human microvascular endothelial cells (HMVEC). Cells were seeded on Collagen I coated 96-well plates at 2.5×10^2 cells/well in assay media. After overnight incubation, VEGF is added to each well in assay media. In general, concentrations from 10^{-7} to 10^{-12} M of each test compound is used. Cells are incubated for 3 days and fresh media containing the various VEGF compounds is added. Cells are assayed by a standard acid phosphatase assay on day 6.

Protein synthesis inhibition is measured in a cell-free system. Samples are diluted in PBS, and 5 μ l of diluted sample is added to 5 μ l of reaction buffer containing 0.25 μ g Brome mosaic virus RNA, 0.5 μ l of a 1 mM amino acid mixture lacking leucine, 12.5 μ Ci 3 H leucine, and 15 μ l of a nuclease-treated rabbit reticulocyte lysate. Samples are incubated for 1 hour at 30°C. The incubation is terminated by the addition of 375 μ l of 1M NaOH in 2% H₂O₂. After 20 minutes, the volume is adjusted to 1.6 ml with H₂O and 50 μ l of the assay mixture, in duplicate, is transferred to a Multiscreen-HA 96 well filtration plate (Millipore, Bedford, MA, U.S.A.). Protein contents of each well were precipitated by adding 250 μ l of ice-cold 30% trichloroacetic acid in 2% casamino acid. After incubation on ice for 30 min, TCA precipitable material was collected by washing the wells three times with 250 μ l of ice cold 5% trichloroacetic acid. After drying, filter paper circles were punched out of the 96-well plate, inserted into vials containing 5 ml of BetaMax scintillation fluid (ICN, Costa Mesa, CA, U.S.A.) and counts were determined using a Beckman LS 6000SC liquid scintillation counter.

As shown in Figure 1, both VEGF₁₂₁ and VEGF₁₆₅ were produced in appreciable quantities at 2 hrs post-induction. Moreover dimerization occurred after refolding (Figure 2). VEGF₁₂₁ and VEGF₁₆₅ purified from inclusion bodies were able to induce proliferation of HMVEC cells as assayed by an acid phosphatase assay. HMVEC were grown for 72 hours in media lacking bFGF but which contained the test compounds in varying concentrations. On day 3 (72 hrs), an acid phosphatase assay was performed following standard procedures. Both the chemical conjugate of insect cell derived VEGF₁₆₅ conjugated to SAP (CCSV) and SAP-VEGF₁₂₁ (FPSV) produced from inclusion bodies in *E. coli* were able to inhibit the proliferation of HMVEC in a dose dependent manner at concentrations as low as 10⁻⁹M as compared to the level of stimulation seen with the addition of VEGF₁₂₁ produced in insect cells. FPSV is a more potent inhibitor of cellular proliferation than CCSV. CCSV = chemical conjugate VEGF₁₆₅-SAP; FPSV = SAP-VEGF₁₂₁ made in *E. coli* from inclusion bodies; VEGF₁₂₁ = insect cell derived; Saporin = SAP. (Figure 7)

Expression of VEGF₁₂₁-SAP and VEGF₁₆₅-SAP was also appreciable in the pP_L- λ system (Figure 4) and dimerized (Figure 5). In addition, VEGF₁₂₁ inhibited protein synthesis in a cell-free system indicating that SAP portion of the conjugate retained its ribosomal inactivating activity. (Figure 6)

EXAMPLE 7

CHEMICAL SYNTHESIS OF VEGF-SAP AND SAP-VEGF

About 50-100 nmol of a VEGF, which is dialyzed against phosphate-buffered saline, is added to about 2.5 mg mono-derivatized SAP (a 1.5 molar excess over the VEGF protein) and left on a rocker platform overnight. The ultraviolet-visible wavelength spectrum is checked in order to determine the extent of reaction by the release of pyridylthione, which adsorbs at 343 nm with a known extinction coefficient. The reaction mixtures are treated for purification in the following manner: reaction mixture is passed over a HiTrap heparin-Sepharose column (1 ml) equilibrated with 0.15 M sodium chloride in buffer A at a flow rate of 0.5 ml/min. The column is washed with 0.6 M NaCl and 1.0 M NaCl in buffer A and the product eluted with 4.0 M NaCl in buffer A. Fractions (0.5 ml) are analyzed by gel electrophoresis and absorbance at 280 nm. Peak tubes were pooled and dialyzed versus 10 mM sodium phosphate, pH 7.5 and applied to a Mono S 5/5 column equilibrated with the same buffer. A 10 ml gradient between 0 and 1.0 M sodium chloride in equilibration buffer are used to elute the product.

EXAMPLE 8

PREPARATION OF VEGF-SAP CONJUGATES THAT CONTAIN LINKERS ENCODING
PROTEASE SUBSTRATES

A. Synthesis of oligos encoding protease substrates

Complementary single-stranded oligos in which the sense strand encodes a protease substrate, have been synthesized either using a cyclone machine (Millipore) according the instructions provided by the manufacturer or, if greater than 80 bases, are made by Midland Certified Reagent Co. (Midland, TX). The following oligos have been synthesized and can be introduced into constructs encoding SAP:VEGF, VEGF:SAP as described above EXAMPLES 3 and 4.

1. Cathepsin B substrate linker:

5'- CCATGGCCCTGGCCCTGGCCCTGGCCCTGCCATGG SEQ ID NO. 38

2. Cathepsin D substrate linker

5'- CCATGGGCGGATCGGGCTTCCTGGGCTTCGGCTTCCTGG

GCTTCGCCATGG -3' SEQ ID NO. 39

3. Trypsin substrate linker

5'- CCATGGGCGGATCGGGCGGTGGGTGCGCTGGTAATAGAGT

CAGAAGATCAGTCGGAAGCAGCCTGTCTTGCGGTGGTCTC
GACCTGCAGG CCATGG-3' SEQ ID NO. 44

4. Gly₄Ser

5'- CCATGGGCGG CGGCGGCTCT GCCATGG -3' SEQ ID NO. 40

5. (Gly₄Ser)₂

5'- CCATGGGCGGCGGCGGCTCTGGCGGCGGCGGCTC
TGCCATGG -3' SEQ ID NO. 41

6. (Ser₄Gly)₄

5'- CCATGGCCTCGTCGTCGTCGGGCTCGTCGTCGTCGGGCT
10 CGTCGTCGTCGGGCTCGTCGTCGTCGGGCGCCATGG -3' SEQ ID NO. 42

7. (Ser₄Gly)₂

5'- CCATGGCCTCGTCGTCGTCGGGCTCGTCGTCGTC
GGGCGCCATGG -3' SEQ ID NO. 43

8. Thrombin substrate linker

15 CTG GTG CCG CGC GGC AGC SEQ ID NO. 45

Leu Val Pro Arg Gly Ser

9. Enterokinase substrate linker

GAC GAC GAC GAC CCA SEQ ID NO. 46

Asp Asp Asp Asp Lys

20 10. Factor Xa substrate

ATC GAA GGT CGT SEQ ID NO. 47

Ile Glu Gly Arg

11. Subtilisin linker

Xaa Ala His Tyr SEQ ID NO. 50, where Xaa is preferably Phe (see SEQ ID NO. 49).

25

B. Preparation of DNA constructs encoding SAP-Linker-VEGF

These constructs are prepared as described above for the SAP-(Gly₄Ser)_x-VEGF conjugates, except that DNA encoding the desired protease substrate is included in place of the DNA encoding (Gly₄Ser)_x.

30

EXAMPLE 9

CAM ASSAY FOR ANGIOGENESIS INHIBITION

35 Materials

Fertilized eggs are supplied by Melody Hill Ranch, Aptos, CA. L-[U-¹⁴C] proline (specific activity, 290 mCi/mmol) is purchased from New England

Nuclear, Boston, MA. Type VII collagenase may be obtained from Sigma Chemical Co., St. Louis, MO. Silicone ring cups are obtained by cutting silicone tubing (3mm diameter) into small "O" rings of 1mm in thickness. These silicone ring cups can be reused many times if they are sterilized prior to each assay.

5

Compound Preparation

VEGF protein and peptide-based compounds are dissolved in water containing 0.5% methyl cellulose for testing. In general, 10 μ l of protein solution is implanted on each CAM.

10

Development of the CAM Assay for Angiogenesis Inhibition

The method of Folkman et al. (*Developmental Biology* 41:391-394, 1974) with minor modifications, is used to cultivate chicken embryos as follows:

Fresh fertile eggs are incubated for three days in a standard egg incubator. On Day 3, eggs are cracked under sterile conditions and embryos are placed into 20 x 100mm plastic petri dishes and cultivated at 37°C in an embryo incubator with a water reservoir on the bottom shelf. Air is continuously bubbled into the water reservoir using a small pump such that the humidity in the incubator is kept constant. On Day 9, a sterile silicone ring cup is placed on each CAM and 0.25 μ Ci of 14 C-proline with or without the test materials dissolved in 0.5% methyl cellulose is delivered into each ring cup in a sterile hood. Ten embryos will be used in all control and test groups. After implantation of test materials, embryos are returned to the incubator and cultivation continued. On Day 12, all embryos are transferred into a cold room at 4-6°C. The antiangiogenic effect of each compound is first examined under the microscope with 6x power followed by collagenase assay to give avascular zone scoring and 14 C-proline incorporation into collagenous protein respectively. All embryos are kept on ice while scoring for avascular zone. Three color photographs will be taken of representative CAMs from each group that demonstrate significant positive responses.

Collagenase Assay for Measurement of 14 C-Proline Incorporation in Collagenous Protein

A piece of CAM 10mm in diameter is cut off under each ring cup and placed in a separate tube. 1.0mL of phosphate-buffered saline (PBS, pH 7.3) containing 0.11 and 0.17mg of cycloheximide and dipyrldyl respectively is added. The tubes are placed in a boiling water bath for 10 minutes and then cooled to room temperature. The PBS in each tube is discarded after centrifugation at 3000 x g for 10 minutes. The CAM residue is washed once with 3mL of 15% TCA followed by 3 x

with 3mL of 5% TCA. Centrifugation is carried out as above between each washing. At this point, all non-protein bound radioactivity is removed and the CAM containing the newly synthesized ^{14}C -collagenous protein is suspended in 0.9mL of 0.1 NaOH and 1.1 mL of HEPES buffer at pH 7.4. The pH of the sample is neutralized with 0.8 N HCl using phenol red as indicator.

To digest the ^{14}C -collagenous protein, 7.5 units of collagenase and 500 nmoles of calcium chloride in 40 micro-liter of HEPES buffer is added to the above samples, and the mixtures are incubated at 37°C for 4 hours. The reaction is stopped by adding 1.0mL of 20% TCA containing 5mg of tannic acid into each tube. After vortexing, the samples are centrifuged at 3000 x g for 10 minutes. An aliquot of the clear supernatant is taken for scintillation counting to quantitate the radiolabeled tripeptides corresponding to basement membrane collagen and other collagenous materials synthesized by the CAM from ^{14}C -proline. The CAM pellets in each tube are solubilized in 0.5mL of 1.0 N NaOH by boiling in a water bath for 5 minutes. An aliquot of the dissolved CAM is used for protein determination using the method of Lowry (*J. Biol. Chem.* 193:265-273, 1951). The radioactivity per mg of protein from the CAM treated with a test compound relative to that from the control CAM gives the percent of inhibition.

Since modifications will be apparent to those of skill in this art, it is intended that this invention be limited only by the scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Barbara A. Sosnowski
Kim Victor
Lou Houston
Michael Nova

(ii) TITLE OF INVENTION: CONJUGATES OF VEGF WITH TARGETED AGENTS

(iii) NUMBER OF SEQUENCES: 103

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Brown, Martin, Haller & McClain
(B) STREET: 1660 Union Street
(C) CITY: San Diego
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 92101-2926

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/213,446
(B) FILING DATE: 15-MAR-1994
(C) CLASSIFICATION:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/213,447
(B) FILING DATE: 15-MAR-1994
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Seidman, Stephanie L.
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 519522

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (619)238-0999
(B) TELEFAX: (619)238-0062

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

101

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 6..11
- (D) OTHER INFORMATION: /standard_name= "EcoRI Restriction Site"

(ix) FEATURE:

- (A) NAME/KEY: sig_peptide
 - (B) LOCATION: 12..30
 - (D) OTHER INFORMATION: /function= "N-terminal extension"
- /product= "Native saporin signal peptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTGCAGAATT CGCATGGATC CTGCTTCAAT

30

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 6..11
- (D) OTHER INFORMATION: /standard_name= "EcoRI Restriction Site"

(ix) FEATURE:

- (A) NAME/KEY: terminator
- (B) LOCATION: 23..25
- (D) OTHER INFORMATION: /note= "Anti-sense stop codon"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 26..30
- (D) OTHER INFORMATION: /note= "Anti-sense to carboxyl terminus of mature peptide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGCAGAATT CGCCTCGTTT GACTACTTTG

30

(D) TOPOLOGY: unknown

(B) LOCATION: 1..804

(D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G4 in Example 1B.2."

(D) OTHER INFORMATION: /product= "Saporin"

GCA TGG ATC CTG CTT CAA TTT TCA GCT TGG ACA ACA ACT GAT GCG GTC 48
Ala Trp Ile Leu Leu Gln Phe Ser Ala Trp Thr Thr Thr Asp Ala Val
-15 -10 -5 1

ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT CAA TAC TCA 96
Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser
5 10 15

TCT TTT GTG GAT AAA ATC CGA AAC AAT GTA AAG GAT CCA AAC CTG AAA 144
Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys
20 25 30

TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT AAA GAA AAA 192
Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys
35 40 45

TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC TCA CTT GGC 240
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly
50 55 60 65

CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA ATG GAT AAC 288
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn
70 75 80

ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT ACT TCC GCC 336
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile Thr Ser Ala

103

85	90	95	
GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT CAG AAA GCT			384
Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala			
100	105	110	
TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT GCC CAG ATA			432
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile			
115	120	125	
ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA			480
Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu			
130	135	140	145
CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA			528
Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys			
150	155	160	
AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA			576
Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Val			
165	170	175	
GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC			624
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro Asn			
180	185	190	
AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT			672
Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg			
195	200	205	
AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT			720
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn			
210	215	220	225
AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG			768
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu			
230	235	240	
CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG			804
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys			
245	250		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..804

(ix) **FEATURE:**

(A) NAME/KEY: misc feature

(B) LOCATION: 1..804

(D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G1 in Example I.B.2."

(ix) **FEATURE:**

(A) NAME/KEY: mat peptide

(B) LOCATION: 46..804

(D) OTHER INFORMATION: /product= "Saporin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCA	TGG	ATC	CTG	CTT	CAA	TTT	TCA	GCT	TGG	ACA	ACA	ACT	GAT	GCG	GTC	48
Ala	Trp	Ile	Leu	Leu	Gln	Phe	Ser	Ala	Trp	Thr	Thr	Thr	Asp	Ala	Val	
-15					-10					-5					1	
ACA	TCA	ATC	ACA	TTA	GAT	CTA	GTA	AAT	CCG	ACC	GCG	GGT	CAA	TAC	TCA	96
Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	
			5					10					15			
TCT	TTT	GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	AAC	CTG	AAA	144
Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	
		20					25					30				
TAC	GGT	GGT	ACC	GAC	ATA	GCC	GTG	ATA	GGC	CCA	CCT	TCT	AAA	GAA	AAA	192
Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	
	35					40					45					
TTC	CTT	AGA	ATT	AAT	TTC	CAA	AGT	TCC	CGA	GGA	ACG	GTC	TCA	CTT	GGC	240
Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	
50					55					60					65	
CTA	AAA	CGC	GAT	AAC	TTG	TAT	GTG	GTC	GCG	TAT	CTT	GCA	ATG	GAT	AAC	288
Leu	Lys	Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	
				70					75					80		
ACG	AAT	GTT	AAT	CGG	GCA	TAT	TAC	TTC	AGA	TCA	GAA	ATT	ACT	TCC	GCC	336
Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr	Ser	Ala	
			85					90					95			
GAG	TTA	ACC	GCC	CTT	TTC	CCA	GAG	GCC	ACA	ACT	GCA	AAT	CAG	AAA	GCT	384
Glu	Leu	Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	
		100					105					110				
TTA	GAA	TAC	ACA	GAA	GAT	TAT	CAG	TCG	ATC	GAA	AAG	AAT	GCC	CAG	ATA	432
Leu	Glu	Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala	Gln	Ile	
	115					120					125					
ACA	CAG	GGA	GAT	AAA	TCA	AGA	AAA	GAA	CTC	GGG	TTG	GGG	ATC	GAC	TTA	480
Thr	Gln	Gly	Asp	Lys	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile	Asp	Leu	
130					135					140					145	
CTT	TTG	ACG	TCC	ATG	GAA	GCA	GTG	AAC	AAG	AAG	GCA	CGT	GTG	GTT	AAA	528

105

Leu	Leu	Thr	Ser	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val	Val	Lys	
				150					155					160		
AAC	GAA	GCT	AGG	TTT	CTG	CTT	ATC	GCT	ATT	CAA	ATG	ACA	GCT	GAG	GTA	576
Asn	Glu	Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Val	
				165				170					175			
GCA	CGA	TTT	CGG	TAC	ATT	CAA	AAC	TTG	GTA	ACT	AAG	AAC	TTC	CCC	AAC	624
Ala	Arg	Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Thr	Lys	Asn	Phe	Pro	Asn	
				180				185					190			
AAG	TTC	GAC	TCG	GAT	AAC	AAG	GTG	ATT	CAA	TTT	GAA	GTC	AGC	TGG	CGT	672
Lys	Phe	Asp	Ser	Asp	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Ser	Trp	Arg	
				195			200					205				
AAG	ATT	TCT	ACG	GCA	ATA	TAC	GGA	GAT	GCC	AAA	AAC	GGC	GTG	TTT	AAT	720
Lys	Ile	Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	
				210			215				220			225		
AAA	GAT	TAT	GAT	TTC	GGG	TTT	GGA	AAA	GTG	AGG	CAG	GTG	AAG	GAC	TTG	768
Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	
				230				235					240			
CAA	ATG	GGA	CTC	CTT	ATG	TAT	TTG	GGC	AAA	CCA	AAG					804
Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys					
				245				250								

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..804

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..804
- (D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G2 in Example I.B.2."

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 46..804
- (D) OTHER INFORMATION: /product= "Saporin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCA	TGG	ATC	CTG	CTT	CAA	TTT	TCA	GCT	TGG	ACA	ACA	ACT	GAT	GCG	GTC	48
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

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AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT      720
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn
210                215                220                225

AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG      768
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu
                230                235                240

CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG      804
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys
                245                250

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 804 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..804

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1..804
- (D) OTHER INFORMATION: /note= "Nucleotide sequence corresponding to the clone M13 mp18-G7 in Example I.B.2."

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 46..804
- (D) OTHER INFORMATION: /product= "Saporin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

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GCA TGG ATC CTG CTT CAA TTT TCA GCT TGG ACA ACA ACT GAT GCG GTC      48
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-15                -10                -5                1

ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT CAA TAC TCA      96
Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser
                5                10                15

TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA AAC CTG AAA      144
Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys
                20                25                30

TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT AAA GAA AAA      192
Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys
                35                40                45

```

108

TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC TCA CTT GGC	240
Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly	
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CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA ATG GAT AAC	288
Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn	
70 75 80	
ACG AAT GTT AAT CGG GCA TAT TAC TTC AGA TCA GAA ATT ACT TCC GCC	336
Thr Asn Val Asn Arg Ala Tyr Tyr Phe Arg Ser Glu Ile Thr Ser Ala	
85 90 95	
GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT CAG AAA GCT	384
Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala	
100 105 110	
TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT GCC CAG ATA	432
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile	
115 120 125	
ACA CAG GGA GAT AAA TCA AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA	480
Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu	
130 135 140 145	
CTT TTG ACG TCC ATG GAA GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA	528
Leu Leu Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys	
150 155 160	
AAC GAA GCT AGA TTC CTT CTT ATC GCT ATT CAG ATG ACG GCT GAG GCA	576
Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala	
165 170 175	
GCA CGA TTT AGG TAC ATA CAA AAC TTG GTA ATC AAG AAC TTT CCC AAC	624
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn	
180 185 190	
AAG TTC AAC TCG GAA AAC AAA GTG ATT CAG TTT GAG GTT AAC TGG AAA	672
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys	
195 200 205	
AAA ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT	720
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn	
210 215 220 225	
AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG	768
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu	
230 235 240	
CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG	804
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
245 250	

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) **FEATURE:**

(A) NAME/KEY: CDS
(B) LOCATION: 1..804

(ix) **FEATURE:**

(A) NAME/KEY: misc_feature
(B) LOCATION: 1..804
(D) OTHER INFORMATION: /note= "Nucleotide sequence
corresponding to the clone M13 mp18-G9 in Example I.B.2."

(ix) **FEATURE:**

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(A) NAME/KEY: mat_peptide
(B) LOCATION: 46..804
(D) OTHER INFORMATION: /product= "Saporin"
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCA	TGG	ATC	CTG	CTT	CAA	TTT	TCA	GCT	TGG	ACA	ACA	ACT	GAT	GCG	GTC	48
Ala	Trp	Ile	Leu	Leu	Gln	Phe	Ser	Ala	Trp	Thr	Thr	Thr	Asp	Ala	Val	
-15					-10					-5					1	
ACA	TCA	ATC	ACA	TTA	GAT	CTA	GTA	AAT	CCG	ACC	GCG	GGT	CAA	TAC	TCA	96
Thr	Ser	Ile	Thr	Leu	Asp	Leu	Val	Asn	Pro	Thr	Ala	Gly	Gln	Tyr	Ser	
			5					10					15			
TCT	TTT	GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	AAC	CTG	AAA	144
Ser	Phe	Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	
		20					25					30				
TAC	GGT	GGT	ACC	GAC	ATA	GCC	GTG	ATA	GGC	CCA	CCT	TCT	AAA	GAA	AAA	192
Tyr	Gly	Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	
	35					40				45						
TTC	CTT	AGA	ATT	AAT	TTC	CAA	AGT	TCC	CGA	GGA	ACG	GTC	TCA	CTT	GGC	240
Phe	Leu	Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	
50					55					60					65	
CTA	AAA	CGC	GAT	AAC	TTG	TAT	GTG	GTC	GCG	TAT	CTT	GCA	ATG	GAT	AAC	288
Leu	Lys	Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	
				70					75					80		
ACG	AAT	GTT	AAT	CGG	GCA	TAT	TAC	TTC	AGA	TCA	GAA	ATT	ACT	TCC	GCC	336
Thr	Asn	Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Arg	Ser	Glu	Ile	Thr	Ser	Ala	
			85					90					95			
GAG	TTA	ACC	GCC	CTT	TTC	CCA	GAG	GCC	ACA	ACT	GCA	AAT	CAG	AAA	GCT	384
Glu	Leu	Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	
		100					105					110				

110

TTA GAA TAC ACA GAA GAT TAT CAG TCG ATT GAA AAG AAT GCC CAG ATA	432
Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile	
115 120 125	
ACA CAA GGA GAT CAA AGT AGA AAA GAA CTC GGG TTG GGG ATT GAC TTA	480
Thr Gln Gly Asp Gln Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu	
130 135 140 145	
CTT TCA ACG TCC ATG GAA GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA	528
Leu Ser Thr Ser Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys	
150 155 160	
GAC GAA GCT AGA TTC CTT CTT ATC GCT ATT CAG ATG ACG GCT GAG GCA	576
Asp Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Ala	
165 170 175	
GCG CGA TTT AGG TAC ATA CAA AAC TTG GTA ATC AAG AAC TTT CCC AAC	624
Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Ile Lys Asn Phe Pro Asn	
180 185 190	
AAG TTC AAC TCG GAA AAC AAA GTG ATT CAG TTT GAG GTT AAC TGG AAA	672
Lys Phe Asn Ser Glu Asn Lys Val Ile Gln Phe Glu Val Asn Trp Lys	
195 200 205	
AAA ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT	720
Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn	
210 215 220 225	
AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG	768
Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu	
230 235 240	
CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG	804
Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
245 250	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 10..15
- (D) OTHER INFORMATION: /standard_name= "Nco I restriction enzyme recognition site"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide

111

(B) LOCATION: 15..22

(D) OTHER INFORMATION: /product= "N-terminus of Saporin protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAACAAGTGC CATGGTCACA TC

22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION: 11..16

(D) OTHER INFORMATION: /standard_name= "Nco I restriction enzyme recognition site."

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 1..10

(D) OTHER INFORMATION: /product= "Carboxy terminus of mature FGF protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTAAGAGCG CCATGGAGA

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..12

(D) OTHER INFORMATION: /product= "Carboxy terminus of wild type FGF"

(ix) FEATURE:

(A) NAME/KEY: misc_recomb

(B) LOCATION: 13..18

(D) OTHER INFORMATION: /standard_name= "Nco I restriction enzyme recognition site"

112

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCT AAG AGC TGACCATGGA GA

21

Ala Lys Ser

1

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..96
- (D) OTHER INFORMATION: /product= "pFGFNcoI"
/note= "Equals the plasmid pFC80 with native PGF
stop codon removed."

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 29..34
- (D) OTHER INFORMATION: /standard_name= "Nco I restriction enzyme
recognition site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTT TTT CTT CCA ATG TCT GCT AAG AGC GCC ATG GAG ATC CGG CTG AAT 48
 Leu Phe Leu Pro Met Ser Ala Lys Ser Ala Met Glu Ile Arg Leu Asn
 1 5 10 15

GGT GCA GTT CTG TAC CGG TTT TCC TGT GCC GTC TTT CAG GAC TCC TGAAATCTT 102
 Gly Ala Val Leu Tyr Arg Phe Ser Cys Ala Val Phe Gln Asp Ser
 20 25 30

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1230

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 1..465
 (D) OTHER INFORMATION: /product= "bFGF"

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
 (B) LOCATION: 472..1230
 (D) OTHER INFORMATION: /product= "Saporin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG GCA GCA GGA TCA ATA ACA ACA TTA CCC GCC TTG CCC GAG GAT GGC	48
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly	
1 5 10 15	
GGC AGC GGC GCC TTC CCG CCC GGC CAC TTC AAG GAC CCC AAG CGG CTG	96
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu	
20 25 30	
TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC GGC CGA	144
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg	
35 40 45	
GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTT CAA CTT	192
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu	
50 55 60	
CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT GCT AAC	240
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn	
65 70 75 80	
CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT AAA TGT	288
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys	
85 90 95	
GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT AAC TAC	336
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr	
100 105 110	
AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA TTG AAA	384
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys	
115 120 125	
CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG CAG AAA	432
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys	
130 135 140	
GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC GCC ATG GTC ACA TCA	480
Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Ala Met Val Thr Ser	
145 150 155 160	
ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT CAA TAC TCA TCT TTT	528
Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe	
165 170 175	

GTG	GAT	AAA	ATC	CGA	AAC	AAC	GTA	AAG	GAT	CCA	AAC	CTG	AAA	TAC	GGT	576
Val	Asp	Lys	Ile	Arg	Asn	Asn	Val	Lys	Asp	Pro	Asn	Leu	Lys	Tyr	Gly	
			180					185					190			
GGT	ACC	GAC	ATA	GCC	GTG	ATA	GGC	CCA	CCT	TCT	AAA	GAA	AAA	TTC	CTT	624
Gly	Thr	Asp	Ile	Ala	Val	Ile	Gly	Pro	Pro	Ser	Lys	Glu	Lys	Phe	Leu	
		195					200					205				
AGA	ATT	AAT	TTC	CAA	AGT	TCC	CGA	GGA	ACG	GTC	TCA	CTT	GGC	CTA	AAA	672
Arg	Ile	Asn	Phe	Gln	Ser	Ser	Arg	Gly	Thr	Val	Ser	Leu	Gly	Leu	Lys	
	210					215					220					
CGC	GAT	AAC	TTG	TAT	GTG	GTC	GCG	TAT	CTT	GCA	ATG	GAT	AAC	ACG	AAT	720
Arg	Asp	Asn	Leu	Tyr	Val	Val	Ala	Tyr	Leu	Ala	Met	Asp	Asn	Thr	Asn	
225					230				235						240	
GTT	AAT	CGG	GCA	TAT	TAC	TTC	AAA	TCA	GAA	ATT	ACT	TCC	GCC	GAG	TTA	768
Val	Asn	Arg	Ala	Tyr	Tyr	Phe	Lys	Ser	Glu	Ile	Thr	Ser	Ala	Glu	Leu	
			245					250					255			
ACC	GCC	CTT	TTC	CCA	GAG	GCC	ACA	ACT	GCA	AAT	CAG	AAA	GCT	TTA	GAA	816
Thr	Ala	Leu	Phe	Pro	Glu	Ala	Thr	Thr	Ala	Asn	Gln	Lys	Ala	Leu	Glu	
			260				265						270			
TAC	ACA	GAA	GAT	TAT	CAG	TCG	ATC	GAA	AAG	AAT	GCC	CAG	ATA	ACA	CAG	864
Tyr	Thr	Glu	Asp	Tyr	Gln	Ser	Ile	Glu	Lys	Asn	Ala	Gln	Ile	Thr	Gln	
		275					280					285				
GGA	GAT	AAA	AGT	AGA	AAA	GAA	CTC	GGG	TTG	GGG	ATC	GAC	TTA	CTT	TTG	912
Gly	Asp	Lys	Ser	Arg	Lys	Glu	Leu	Gly	Leu	Gly	Ile	Asp	Leu	Leu	Leu	
	290					295					300					
ACG	TTC	ATG	GAA	GCA	GTG	AAC	AAG	AAG	GCA	CGT	GTG	GTT	AAA	AAC	GAA	960
Thr	Phe	Met	Glu	Ala	Val	Asn	Lys	Lys	Ala	Arg	Val	Val	Lys	Asn	Glu	
305					310				315						320	
GCT	AGG	TTT	CTG	CTT	ATC	GCT	ATT	CAA	ATG	ACA	GCT	GAG	GTA	GCA	CGA	1008
Ala	Arg	Phe	Leu	Leu	Ile	Ala	Ile	Gln	Met	Thr	Ala	Glu	Val	Ala	Arg	
			325					330					335			
TTT	AGG	TAC	ATT	CAA	AAC	TTG	GTA	ACT	AAG	AAC	TTC	CCC	AAC	AAG	TTC	1056
Phe	Arg	Tyr	Ile	Gln	Asn	Leu	Val	Thr	Lys	Asn	Phe	Pro	Asn	Lys	Phe	
			340					345					350			
GAC	TCG	GAT	AAC	AAG	GTG	ATT	CAA	TTT	GAA	GTC	AGC	TGG	CGT	AAG	ATT	1104
Asp	Ser	Asp	Asn	Lys	Val	Ile	Gln	Phe	Glu	Val	Ser	Trp	Arg	Lys	Ile	
		355					360					365				
TCT	ACG	GCA	ATA	TAC	GGG	GAT	GCC	AAA	AAC	GGC	GTG	TTT	AAT	AAA	GAT	1152
Ser	Thr	Ala	Ile	Tyr	Gly	Asp	Ala	Lys	Asn	Gly	Val	Phe	Asn	Lys	Asp	
		370				375					380					
TAT	GAT	TTC	GGG	TTT	GGA	AAA	GTG	AGG	CAG	GTG	AAG	GAC	TTG	CAA	ATG	1200
Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	Lys	Asp	Leu	Gln	Met	
385					390				395						400	

115

GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG 1230
 Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys
 405 410

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1230

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 1..465
- (D) OTHER INFORMATION: /product= "bFGF"

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 472..1230
- (D) OTHER INFORMATION: /product= "Saporin"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GCT GCT GGT TCT ATC ACT ACT CTG CCG GCT CTG CCG GAA GAC GGT	48
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly	
1 5 10 15	
GGT TCT GGT GCT TTC CCG CCC GGC CAC TTC AAG GAC CCC AAG CGG CTG	96
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu	
20 25 30	
TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC GGC CGA	144
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg	
35 40 45	
GTC GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTT CAA CTT	192
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu	
50 55 60	
CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT GCT AAC	240
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn	
65 70 75 80	
CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT AAA TGT	288
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys	
85 90 95	

116

GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT AAC TAC Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr 100 105 110	336
AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA TTG AAA Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys 115 120 125	384
CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG CAG AAA Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys 130 135 140	432
GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC GCC ATG GTC ACA TCA Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser Ala Met Val Thr Ser 145 150 155 160	480
ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT CAA TAC TCA TCT TTT Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe 165 170 175	528
GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA AAC CTG AAA TAC GGT Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly 180 185 190	576
GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT AAA GAA AAA TTC CTT Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu 195 200 205	624
AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC TCA CTT GGC CTA AAA Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys 210 215 220	672
CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA ATG GAT AAC ACG AAT Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn 225 230 235 240	720
GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT ACT TCC GCC GAG TTA Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile Thr Ser Ala Glu Leu 245 250 255	768
ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT CAG AAA GCT TTA GAA Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu 260 265 270	816
TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT GCC CAG ATA ACA CAG Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln 275 280 285	864
GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA CTT TTG Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Leu 290 295 300	912
ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA AAC GAA Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg Val Val Lys Asn Glu	960

117

305	310	315	320	
GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA GCA CGA				1008
Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala Arg				
	325	330	335	
TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC AAG TTC				1056
Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe				
	340	345	350	
GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT				1104
Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile				
	355	360	365	
TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT				1152
Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp				
	370	375	380	
TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG				1200
Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met				
	385	390	395	400
GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG				1230
Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys				
	405	410		

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= trp promoter

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

AATTCCTG TTGACAATTA ATCATCGAAC TAGTTAACTA GTACGCAGCT TGGCTGCAG 59

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

(D) OTHER INFORMATION/product= bacteriophage lambda cII ribosome binding site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTCGACCAAG CTTGGGCATA CATTCAATCA ATTGTTATCT AAGGAAATAC TTACATATG 59

(2) INFORMATION FOR SEQ ID NO:16

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..66
- (D) OTHER INFORMATION: /product= VEGF gene EXON I (VEGF LEADER SEQUENCE -26 - -5)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16

ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC TTG CTG CTC 48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu Leu
1 5 10 15

TAC CTC CAC CAT GCC AAG 66
Tyr Leu His His Ala Lys
20

(2) INFORMATION FOR SEQ ID NO:17

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..52
- (D) OTHER INFORMATION: /product= VEGF gene EXON II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17

TGG TCC CAG GCT GCA CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC 48
Trp Ser Gln Ala Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His
1 5 10 15

GAA G 52
Glu

(2) INFORMATION FOR SEQ ID NO:18

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..197
- (D) OTHER INFORMATION: /product= VEGF gene EXON III

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18

TG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC	47
Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile	
1 5 10 15	
GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC	95
Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr	
20 25 30	
ATC TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC	143
Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys	
35 40 45	
AAT GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC	191
Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr	
50 55 60	
ATG CAG	197
Met Gln	
64	

(2) INFORMATION FOR SEQ ID NO:19

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..75
- (D) OTHER INFORMATION: /product= VEGF gene EXON IV

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19

ATT ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC	48
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120

Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser
 110 115 120

TTC CTA CAG CAC AAC AAA TGT GAA TGC AG 77
 Phe Leu Gln His Asn Lys Cys Glu Cys
 125 130 135 140

(2) INFORMATION FOR SEQ ID NO:20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..27
- (D) OTHER INFORMATION: /product= VEGF gene EXON V

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20

A CCA AAG AAA GAT AGA GCA AGA CAA GAA AA 30
 Pro Lys Lys Asp Arg Ala Arg Gln Glu
 5

(2) INFORMATION FOR SEQ ID NO:21

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..70
- (D) OTHER INFORMATION: /product= VEGF gene EXON VI

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21

A AAA TCA GTT CGA GGA AAG GGA AAG GGG CAA AAA CGA AAG CGC AAG AAA 49
 Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys
 1 5 10 15

TCC CGG TAT AAG TCC TGG AGC GT 72
 Ser Arg Tyr Lys Ser Trp Ser
 20

(2) INFORMATION FOR SEQ ID NO:22

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) **FEATURE:**

- (A) NAME/KEY: CDS
(B) LOCATION: 1..51
(D) OTHER INFORMATION: /product= Insert between EXON VI & VII

(xi) SEQUENCE DESCRIPTION: SEO ID NO:22

TAC	GTT	GGT	GCC	CGC	TGC	TGT	CTA	ATG	CCC	TGG	AGC	CTC	CCT	GGC	CCC	48
Tyr	Val	Gly	Ala	Arg	Cys	Cys	Leu	Met	Pro	Trp	Ser	Leu	Pro	Gly	Pro	
1				5					10					15		
CAT																51
His																

(2) INFORMATION FOR SEQ ID NO:23

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 2..130
(D) OTHER INFORMATION: /product= EXON VII

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23

T	CCC	TGT	GGG	CCT	TGC	TCA	GAG	CGG	AGA	AAG	CAT	TTG	TTT	GTA	CAA	GAT	49
	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln	Asp	
	1				5					10					15		
CCG	CAG	ACG	TGT	AAA	TGT	TCC	TGC	AAA	AAC	ACA	GAC	TCG	CGT	TGC	AAG	97	
Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	Lys		
			20					25					30				
GCG	AGG	CAG	CTT	GAG	TTA	AAC	GAA	CGT	ACT	TGC	AG					132	
Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys							
		35				40											

(2) INFORMATION FOR SEQ ID NO:24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

122

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: genomic

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 2..19
 (D) OTHER INFORMATION: /product= EXON VIII

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24

A TGT GAC AAG CCG AGG CGG TGA
 Cys Asp Lys Pro Arg Arg
 1 5

22

(2) INFORMATION FOR SEQ ID NO:25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 13..456
 (D) OTHER INFORMATION: /product= "VEGF₁₂₁-encoding DNA"

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 13..90
 (D) OTHER INFORMATION: /product= leader-encoding sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25

GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT
 Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu
 1 5 10

48

GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC
 Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro
 15 20 25

96

ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG
 Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met
 30 35 40

144

GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC
 Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp
 45 50 55 60

192

123

ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC	240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	
65 70 75	
TGT GTG CCC CTG ATG CGA TGC GGC GGC TGC TGC AAT GAC GAG GGC CTG	288
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG	336
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG	384
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA	432
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
AAA TGT GAC AAG CCG AGG CGG TGATGAATGA ATGAGGATCC	473
Lys Cys Asp Lys Pro Arg Arg	
145	

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 605 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..588
- (D) OTHER INFORMATION: /product= "VEGF₁₆₅-encoding DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..90
- (D) OTHER INFORMATION: /product= "leader sequence-encoding DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT	48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu	
1 5 10	
GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC	96
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro	

124

15	20	25	
ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG			144
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met			
30	35	40	
GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC			192
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp			
45	50	55	60
ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC			240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser			
65	70	75	
TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG			288
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu			
80	85	90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG			336
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg			
95	100	105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG			384
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln			
110	115	120	
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA			432
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu			
125	130	135	140
AAT CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA			480
Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln			
145	150	155	
GAT CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC			528
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys			
160	165	170	
AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC AAG			576
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys			
175	180	185	
CCG AGG CGG TGATGAATGA ATGAGGATCC			605
Pro Arg Arg			
190			

(2) INFORMATION FOR SEQ ID NO:27

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 677 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 13..657

(D) OTHER INFORMATION: /product= "VEGF₁₈₉-encoding DNA"

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 13..90

(D) OTHER INFORMATION: /product= "leader sequence-encoding DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27

GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT	48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu	
1 5 10	
GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC	96
Ala Leu Leu Leu Tyr Leu His Ala Lys Trp Ser Gln Ala Ala Pro	
15 20 25	
ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG	144
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met	
30 35 40	
GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC	192
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp	
45 50 55 60	
ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC	240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	
65 70 75	
TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG	288
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG	336
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG	384
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAG GAT AGA GCA AGA CAA GAA	432
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
AAA AAA TCA GTT CGA GGA AAG GGA AAG GGG CAA AAA CGA AAG CGC AAG	480
Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys	
145 150 155	
AAA TCC CGG TAT AAG TCC TGG AGC GTT CCC TGT GGG CCT TGC TCA GAG	528
Lys Ser Arg Tyr Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu	

126

160	165	170	
CGG AGA AAG CAT TTG TTT GTA CAA GAT CCG CAG ACG TGT AAA TGT TCC			576
Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser			
175	180	185	
TGC AAA AAC ACA GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG TTA AAC			624
Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn			
190	195	200	
GAA CGT ACT TGC AGA TGT GAC AAG CCG AGG CGG TGATGAATGA ATGAGGATCC			677
Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg			
205	210	215	

(2) INFORMATION FOR SEQ ID NO:28

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 728 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..711
- (D) OTHER INFORMATION: /product= "VEGF206-encoding DNA"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 13..90
- (D) OTHER INFORMATION: /product= leader sequence encoding DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28

GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT	48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu	
1 5 10	
GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC	96
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro	
15 20 25	
ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG	144
Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met	
30 35 40	
GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC	192
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp	
45 50 55 60	
ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC	240
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	
65 70 75	

127

TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG	288
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu	
80 85 90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG	336
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg	
95 100 105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG	384
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln	
110 115 120	
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAG GAT AGA GCA AGA CAA GAA	432
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu	
125 130 135 140	
AAA AAA TCA GTT CGA GGA AAG GGA AAG GGG CAA AAA CGA AAG CGC AAG	480
Lys Lys Ser Val Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys	
145 150 155	
AAA TCC CGG TAT AAG TCC TGG AGC GTT TAC GTT GGT GCC CGC TGC TGT	528
Lys Ser Arg Tyr Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys	
160 165 170	
CTA ATG CCC TGG AGC CTC CCT GGC CCC CAT CCC TGT GGG CCT TGC TCA	576
Leu Met Pro Trp Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser	
175 180 185	
GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT CCG CAG ACG TGT AAA TGT	624
Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys	
190 195 200	
TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG TTA	672
Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu	
205 210 215 220	
AAC GAA CGT ACT TGC AGA TGT GAC AAG CCG AGG CGG TGATGAATGA	718
Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg	
225 230 235	
ATGAGGATCC	728

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 4..768
 (D) OTHER INFORMATION: /product= "SAP CYS +4"

(ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 7..768
 (D) OTHER INFORMATION: /product= "mature SAP CYS +4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAT ATG GTC ACA TCA TGT ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT	48
Met Val Thr Ser Cys Thr Leu Asp Leu Val Asn Pro Thr Ala Gly	
1 5 10 15	
CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA	96
Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro	
20 25 30	
AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT	144
Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	
35 40 45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC	192
Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	
50 55 60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA	240
Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	
65 70 75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT	288
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	
80 85 90 95	
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT	336
Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	
100 105 110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT	384
Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	
115 120 125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG	432
Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	
130 135 140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT	480
Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	
145 150 155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA	528
Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	
160 165 170 175	

GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC	576
Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn	
180 185 190	
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC	624
Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val	
195 200 205	
AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC	672
Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly	
210 215 220	
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG	720
Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val	
225 230 235	
AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG TAG	768
Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
240 245 250 255	

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..768
- (D) OTHER INFORMATION: /product= "SAP CYS +10"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 7..768
- (D) OTHER INFORMATION: /product= "mature SAP CYS +10"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA TGT CCG ACC GCG GGT	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Cys Pro Thr Ala Gly	
1 5 10 15	
CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA	96
Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro	
20 25 30	
AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT	144

130

Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	
35 40 45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC	192
Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	
50 55 60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA	240
Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	
65 70 75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT	288
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	
80 85 90 95	
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT	336
Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	
100 105 110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT	384
Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	
115 120 125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG	432
Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	
130 135 140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT	480
Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	
145 150 155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA	528
Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	
160 165 170 175	
GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC	576
Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn	
180 185 190	
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC	624
Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val	
195 200 205	
AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC	672
Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly	
210 215 220	
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG	720
Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val	
225 230 235	
AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG TAG	768
Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
240 245 250 255	

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1212
- (D) OTHER INFORMATION: /product= "VEGF121-SAP LEADER pZ1B"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..81
- (D) OTHER INFORMATION: /product= "LEADER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CAT ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC TTG CTG	48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala Leu Leu	
1 5 10 15	
CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCA ATG GCA GAA	96
Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu	
20 25 30	
GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT GTC TAT	144
Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr	
35 40 45	
CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG	192
Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln	
50 55 60	
GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC	240
Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro	
65 70 75	
CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG	288
Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val	
80 85 90 95	
CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT	336
Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro	
100 105 110	
CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC AAC AAA	384
His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys	

132

115	120	125	
TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAA TGT GAC			432
Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp			
130	135	140	
AAG CCG AGG CGG CCA TGG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT			480
Lys Pro Arg Arg Pro Trp Val Thr Ser Ile Thr Leu Asp Leu Val Asn			
145	150	155	
CCG ACC GCG GGT CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC			528
Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn			
160	165	170	175
GTA AAG GAT CCA AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA			576
Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile			
180	185	190	
GGC CCA CCT TCT AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC			624
Gly Pro Pro Ser Lys Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser			
195	200	205	
CGA GGA ACG GTC TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC			672
Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val			
210	215	220	
GCG TAT CTT GCA ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC			720
Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe			
225	230	235	
AAA TCA GAA ATT ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC			768
Lys Ser Glu Ile Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala			
240	245	250	255
ACA ACT GCA AAT CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG			816
Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser			
260	265	270	
ATC GAA AAG AAT GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA			864
Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu			
275	280	285	
CTC GGG TTG GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC			912
Leu Gly Leu Gly Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn			
290	295	300	
AAG AAG GCA CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT			960
Lys Lys Ala Arg Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala			
305	310	315	
ATT CAA ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG			1008
Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu			
320	325	330	335
GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT			1056

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Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile	
340 345 350	
CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT	1104
Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp	
355 360 365	
GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA	1152
Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys	
370 375 380	
GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC	1200
Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly	
385 390 395	
AAA CCA AAG TAG	1212
Lys Pro Lys	
400	

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1269
- (D) OTHER INFORMATION: /product= "VEGF165-SAP NO LEADER pZ1B"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CAT ATG GCA CCA ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG	48
Met Ala Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val	
1 5 10 15	
GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG	96
Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu	
20 25 30	
ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC	144
Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile	
35 40 45	
TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT	192
Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn	
50 55 60	

GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG	240
Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met	
65 70 75	
CAG ATT ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG	288
Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met	
80 85 90 95	
AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA	336
Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg	
100 105 110	
GCA AGA CAA GAA AAT CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT	384
Ala Arg Gln Glu Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His	
115 120 125	
TTG TTT GTA CAA GAT CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA	432
Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr	
130 135 140	
GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC	480
Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys	
145 150 155	
AGA TGT GAC AAG CCG AGG CGG CCA TGG GTC ACA TCA ATC ACA TTA GAT	528
Arg Cys Asp Lys Pro Arg Arg Pro Trp Val Thr Ser Ile Thr Leu Asp	
160 165 170 175	
CTA GTA AAT CCG ACC GCG GGT CAA TAC TCA TCT TTT GTG GAT AAA ATC	576
Leu Val Asn Pro Thr Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys Ile	
180 185 190	
CGA AAC AAC GTA AAG GAT CCA AAC CTG AAA TAC GGT GGT ACC GAC ATA	624
Arg Asn Asn Val Lys Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp Ile	
195 200 205	
GCC GTG ATA GGC CCA CCT TCT AAA GAA AAA TTC CTT AGA ATT AAT TTC	672
Ala Val Ile Gly Pro Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn Phe	
210 215 220	
CAA AGT TCC CGA GGA ACG GTC TCA CTT GGC CTA AAA CGC GAT AAC TTG	720
Gln Ser Ser Arg Gly Thr Val Ser Leu Gly Leu Lys Arg Asp Asn Leu	
225 230 235	
TAT GTG GTC GCG TAT CTT GCA ATG GAT AAC ACG AAT GTT AAT CGG GCA	768
Tyr Val Val Ala Tyr Leu Ala Met Asp Asn Thr Asn Val Asn Arg Ala	
240 245 250 255	
TAT TAC TTC AAA TCA GAA ATT ACT TCC GCC GAG TTA ACC GCC CTT TTC	816
Tyr Tyr Phe Lys Ser Glu Ile Thr Ser Ala Glu Leu Thr Ala Leu Phe	
260 265 270	
CCA GAG GCC ACA ACT GCA AAT CAG AAA GCT TTA GAA TAC ACA GAA GAT	864
Pro Glu Ala Thr Thr Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu Asp	
275 280 285	

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TAT CAG TCG ATC GAA AAG AAT GCC CAG ATA ACA CAG GGA GAT AAA AGT	912
Tyr Gln Ser Ile Glu Lys Asn Ala Gln Ile Thr Gln Gly Asp Lys Ser	
290 295 300	
AGA AAA GAA CTC GGG TTG GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA	960
Arg Lys Glu Leu Gly Leu Gly Ile Asp Leu Leu Leu Thr Phe Met Glu	
305 310 315	
GCA GTG AAC AAG AAG GCA CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG	1008
Ala Val Asn Lys Lys Ala Arg Val Val Lys Asn Glu Ala Arg Phe Leu	
320 325 330 335	
CTT ATC GCT ATT CAA ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT	1056
Leu Ile Ala Ile Gln Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile	
340 345 350	
CAA AAC TTG GTA ACT AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC	1104
Gln Asn Leu Val Thr Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn	
355 360 365	
AAG GTG ATT CAA TTT GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA	1152
Lys Val Ile Gln Phe Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile	
370 375 380	
TAC GGG GAT GCC AAA AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG	1200
Tyr Gly Asp Ala Lys Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly	
385 390 395	
TTT GGA AAA GTG AGG CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG	1248
Phe Gly Lys Val Arg Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met	
400 405 410 415	
TAT TTG GGC AAA CCA AAG TAG	1269
Tyr Leu Gly Lys Pro Lys	
420	

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..1352
- (D) OTHER INFORMATION: /product= "VEGF165-SAP LEADER BAC"

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..89

(D) OTHER INFORMATION: /product= "LEADER"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC	50
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala	
1 5 10	
TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCA ATG	98
Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met	
15 20 25	
GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT	146
Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp	
30 35 40 45	
GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC	194
Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile	
50 55 60	
TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT	242
Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys	
65 70 75	
GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG	290
Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu	
80 85 90	
TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC	338
Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile	
95 100 105	
AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC	386
Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His	
110 115 120 125	
AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAT	434
Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn	
130 135 140	
CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT	482
Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp	
145 150 155	
CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG	530
Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys	
160 165 170	
GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC AAG CCG	578
Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro	
175 180 185	
AGG CGG CCA TGG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC	626
Arg Arg Pro Trp Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr	

190	195	200	205	
GCG GGT CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG				674
Ala Gly Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys	210	215	220	
GAT CCA AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA				722
Asp Pro Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro	225	230	235	
CCT TCT AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA				770
Pro Ser Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly	240	245	250	
ACG GTC TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT				818
Thr Val Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr	255	260	265	
CTT GCA ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA				866
Leu Ala Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser	270	275	280	285
GAA ATT ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT				914
Glu Ile Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr	290	295	300	
GCA AAT CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA				962
Ala Asn Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu	305	310	315	
AAG AAT GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG				1010
Lys Asn Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly	320	325	330	
TTG GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG				1058
Leu Gly Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys	335	340	345	
GCA CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA				1106
Ala Arg Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln	350	355	360	365
ATG ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT				1154
Met Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr	370	375	380	
AAG AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT				1202
Lys Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe	385	390	395	
GAA GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA				1250
Glu Val Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys	400	405	410	
AAC GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG				1298

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Asn Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg
 415 420 425

CAG GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA 1346
 Gln Val Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro
 430 435 440 445

AAG TAGTCAAACG AGGCCTGCAG 1369
 Lys

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

CATATGTGTGTCACATCAATCACATTAGAT 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

CAGGTTTGGA TCCTTTACGT T 21

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36

AAGGAGATATACC ATG GGC AGC AGC CAT CAT CAT CAT CAT CAC AGC AGC 43
 Met Gly Ser Ser His His His His His His Ser Ser
 1 5 10

GGC CTG GTG CCG CGC GGC AGC CAT ATG CTC GAG GAT CCG 82
 Gly Leu Val Pro Arg Gly Ser His Met Leu Glu Asp Pro
 15 20 25

(2) INFORMATION FOR SEQ ID NO:37:

139

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37

AAA CAACGTAAA AGA TCCAAA CCTGAAA

23

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..35
- (A) NAME/KEY: Cathepsin B linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38

CCATGGCCCT GGCCCTGGCC CTGGCCCTGG CCATGG

36

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..50
- (A) NAME/KEY: Cathepsin D linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39

CCATGGGCCG ATCGGGCTTC CTGGGCTTCG GCTTCCTGGG CTCGCCATGG

51

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs

140

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..26
- (A) NAME/KEY: Gly₄Ser with NcoI ends

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40

CCATGGGCGG CGGCGGCTCT GCCATGG

27

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..41
- (A) NAME/KEY: (Gly₄Ser)₂ with NcoI ends

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41

CCATGGGCGG CGGCGGCTCT GCGGCGGCG GCTCTGCCAT GG

42

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..74
- (A) NAME/KEY: (Ser₄Gly)₄ with NcoI ends

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42

CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCTC GTCGTCGTCG GGCTCGTCGT

60

CGTCGGGCGC CATGG

75

141

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..45
- (A) NAME/KEY: (Ser₄Gly)₂

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43

CCATGGCCTC GTCGTCGTCG GGCTCGTCGT CGTCGGGCGC CATGG

45

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 3..95
- (A) NAME/KEY: "Trypsin linker"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44

CCATGGGCCG ATCGGGCGGT GGGTGCGCTG GTAATAGAGT CAGAAGATCA GTCGGAAGCA

60

GCCTGTCTTG CGGTGGTCTC GACCTGCAGG CCATGG

96

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18
- (D) OTHER INFORMATION: /product= Thrombin substrate linker

142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45

CTG GTG CCG CGC GGC AGC
Leu Val Pro Arg Gly Ser
1 5

18

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..15
- (D) OTHER INFORMATION: /product= Enterokinase substrate linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46

GAC GAC GAC GAC CCA
Asp Asp Asp Asp Lys
1 5

15

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..12
- (D) OTHER INFORMATION: /product= Factor Xa substrate

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47

ATC GAA GGT CGT
Ile Glu Gly Arg
1

12

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

143

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..8

(D) OTHER INFORMATION: /product= Flexible linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48

Ala Ala Pro Ala Ala Ala Pro Ala

1

5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /product= subtilisin substrate linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49

Phe Ala His Tyr

1

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..4

(D) OTHER INFORMATION: /product= subtilisin substrate linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50

Xaa Asp Glu Leu

1

4

(2) INFORMATION FOR SEQ ID NO:51:

144

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51

CCATGGCACC AATGGCAGAA GGAGGA

26

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52

GTCGACTCAT CACCGCCTCG GCTT

24

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53

CCATGGGCGG CGGCGGCTCT GCACCAATGG CAGAAGGA

38

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54

CCATGGGCGG CGGCGGCTCT GCGGCGGCG GCTCTGCACC AATGGCAGAA GGA

53

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55

CCATGGCAGA GCCGCCGCCG CCCCGCCTCG GCTTGTCACA T

41

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56

CCATGGCAGA GCCGCCGCCG CCAGAGCCGC CGCCGCCCCG CCTCGGCTTG TCACAT

56

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1155
- (D) OTHER INFORMATION: /product= "SAP-(Gly4Ser)-VEGF121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT
 Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly
 1 5 10 15

48

CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA
 Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro
 20 25 30

96

AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	144
35 40 45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	192
50 55 60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	240
65 70 75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	288
80 85 90 95	
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	336
100 105 110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	384
115 120 125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	432
130 135 140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	480
145 150 155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	528
160 165 170 175	
GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn	576
180 185 190	
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val	624
195 200 205	
AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly	672
210 215 220	
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val	720
225 230 235	
AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG GCC Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ala	768

147

240	245	250	255	
ATG GGC GGC GGC GGC TCT GCC ATG GCA CCA ATG GCA GAA GGA GGA GGG				816
Met Gly Gly Gly Gly Ser Ala Met Ala Pro Met Ala Glu Gly Gly Gly				
	260	265	270	
CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC				864
Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser				
	275	280	285	
TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT				912
Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro				
	290	295	300	
GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA				960
Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg				
	305	310	315	
TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG				1008
Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu				
	320	325	330	335
GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT CAC CAA GGC				1056
Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly				
	340	345	350	
CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC				1104
Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys				
	355	360	365	
AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAA TGT GAC AAG CCG AGG				1152
Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg				
	370	375	380	
CGG TGATGAGTCG AC				1167
Arg				

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1287
- (D) OTHER INFORMATION: /product= "SAP-(Gly4Ser)-VEGF165"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly	
1 5 10 15	
CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA	96
Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro	
20 25 30	
AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT	144
Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	
35 40 45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC	192
Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	
50 55 60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA	240
Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	
65 70 75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT	288
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	
80 85 90 95	
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT	336
Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	
100 105 110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT	384
Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	
115 120 125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG	432
Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	
130 135 140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT	480
Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	
145 150 155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA	528
Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	
160 165 170 175	
GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC	576
Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn	
180 185 190	
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC	624
Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val	
195 200 205	

149

AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly 210 215 220	672
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val 225 230 235	720
AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG GCC Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ala 240 245 250 255	768
ATG GGC GGC GGC GGC TCT GCC ATG GCA CCA ATG GCA GAA GGA GGA GGC Met Gly Gly Gly Gly Ser Ala Met Ala Pro Met Ala Glu Gly Gly Gly 260 265 270	816
CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser 275 280 285	864
TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro 290 295 300	912
GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg 305 310 315	960
TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu 320 325 330 335	1008
GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT CAC CAA GGC Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly 340 345 350	1056
CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys 355 360 365	1104
AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAT CCC TGT GGG CCT TGC Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Asn Pro Cys Gly Pro Cys 370 375 380	1152
TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA GAT CCG CAG ACG TGT AAA Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys 385 390 395	1200
TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu 400 405 410 415	1248
TTA AAC GAA CGT ACT TGC AGA TGT GAC AAG CCG AGG CCG TGATGAGTCG Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys Pro Arg Arg 420 425	1297

AC

1299

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..771
- (D) OTHER INFORMATION: /product= "SAP CYS -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CAT ATG TGT GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG	48
Met Cys Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala	
1 5 10 15	
GGT CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT	96
Gly Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp	
20 25 30	
CCA AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT	144
Pro Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro	
35 40 45	
TCT AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG	192
Ser Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr	
50 55 60	
GTC TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT	240
Val Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu	
65 70 75	
GCA ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA	288
Ala Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu	
80 85 90 95	
ATT ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA	336
Ile Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala	
100 105 110	
AAT CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG	384
Asn Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys	
115 120 125	

151

AAT GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG	432
Asn Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu	
130 135 140	
GGG ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA	480
Gly Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala	
145 150 155	
CGT GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG	528
Arg Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met	
160 165 170 175	
ACA GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG	576
Thr Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys	
180 185 190	
AAC TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA	624
Asn Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu	
195 200 205	
GTC AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC	672
Val Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn	
210 215 220	
GGC GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG	720
Gly Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln	
225 230 235	
GTG AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG	768
Val Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys	
240 245 250 255	
TAG	771

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

TCCCAGGCTG CACCAATGGC AGAAGGAGGA

30

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

152

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1-9

(D) OTHER INFORMATION: /product= "3' linking oligo for insertion into 11a/15b"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

TCCTCCTTCT GCCATTGGTG CAGCCTGGGA

30

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CATATGAACT TTCTGCTGTC TTGG

24

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 29 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATATGGCAC CAATGGCAGA AGGAGGAGG

29

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGATCCTCAT CACCGCCTCG GCTT

24

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

CCATGGCCGC CTCGGCTTGT C

21

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGATCCGAAA CATGAACTTT CTGCTGTCT

29

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GGATCCGAAA CATATGAACT TTCTGCTGTC T

31

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CTGCAGTCAT CACCGCCTCG GCTT

24

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

CATATGGTCA CATCATGTAC ATTAGATCTA GTAAAT

36

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CATATGGTCA CATCAATCAC ATTAGATCTA GTATGTCCGA CCGCGGGTCA

50

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

CTGCAGGCCT CGTTTGACTA CTT

23

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: p ptide

(ix) FEATURE:

155

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72

Ala Pro Arg Arg Arg Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

TTTCAGGTTT GGATCTTTTA CGTTGTTT

28

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GGATCCGCCT CGTTTGACTA CTT

23

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75

Ile Lys Arg Leu Arg Arg

1

5

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76

Ile Lys Arg Gln Arg Arg

1

5

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (D) OTHER INFORMATION: /product= "SO-4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Ile Ty Glu Leu Asn Leu Gln Gly Thr Thr Lys Ala Gln Tyr

5

10

15

Ser Thr Ile Leu Lys Gln Leu Arg Asp Asp Ile Lys Asp Pro Asn Leu

20

25

30

Xaa Tyr Gly Xaa Xaa Asp Tyr Ser

35

40

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

157

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..1545

(D) OTHER INFORMATION: /product=

"SAP-(Gly4Ser)-VEGF121-(Gly4Ser)-VEGF121"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly	
1 5 10 15	
CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA	96
Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro	
20 25 30	
AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT	144
Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	
35 40 45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC	192
Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	
50 55 60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA	240
Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	
65 70 75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT	288
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	
80 85 90 95	
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT	336
Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	
100 105 110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT	384
Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	
115 120 125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG	432
Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	
130 135 140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT	480
Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	
145 150 155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA	528
Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	
160 165 170 175	

158

GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn 180 185 190	576
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val 195 200 205	624
AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC Ser Trp Arg Lys Ile Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly 210 215 220	672
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG Val Phe Asn Lys Asp Tyr Asp Phe Gly Phe Gly Lys Val Arg Gln Val 225 230 235	720
AAG GAC TTG CAA ATG GGA CTC CTT ATG TAT TTG GGC AAA CCA AAG GCC Lys Asp Leu Gln Met Gly Leu Leu Met Tyr Leu Gly Lys Pro Lys Ala 240 245 250 255	768
ATG GGC GGC GGC GGC TCT GCC ATG GCA CCA ATG GCA GAA GGA GGA GGG Met Gly Gly Gly Gly Ser Ala Met Ala Pro Met Ala Glu Gly Gly Gly 260 265 270	816
CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln Arg Ser 275 280 285	864
TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro 290 295 300	912
GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu Met Arg 305 310 315	960
TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro Thr Glu 320 325 330 335	1008
GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT CAC CAA GGC Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His Gln Gly 340 345 350	1056
CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys Glu Cys 355 360 365	1104
AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAA TGT GAC AAG CCG AGG Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys Pro Arg 370 375 380	1152
CGG GCC ATG GGC GGC GGC GGC TCT GCC ATG GCA CCA ATG GCA GAA GGA Arg Ala Met Gly Gly Gly Gly Ser Ala Met Ala Pro Met Ala Glu Gly 385 390 395	1200

159

GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG GAT GTC TAT CAG	1248
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
400 405 410 415	
CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC ATC TTC CAG GAG	1296
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu	
420 425 430	
TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC TGT GTG CCC CTG	1344
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu	
435 440 445	
ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG GAG TGT GTG CCC	1392
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro	
450 455 460	
ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG ATC AAA CCT CAC	1440
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His	
465 470 475	
CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG CAC AAC AAA TGT	1488
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys	
480 485 490 495	
GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA AAA TGT GAC AAG	1536
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys	
500 505 510	
CCG AGG CGG TGATGAGTCG AC	1557
Pro Arg Arg	

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1809 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..1797
- (D) OTHER INFORMATION: /product=
"SAP- (Gly4Ser)-VEGF165- (Gly4Ser)-VEGF165"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CAT ATG GTC ACA TCA ATC ACA TTA GAT CTA GTA AAT CCG ACC GCG GGT	48
Met Val Thr Ser Ile Thr Leu Asp Leu Val Asn Pro Thr Ala Gly	

160

1	5	10	15	
CAA TAC TCA TCT TTT GTG GAT AAA ATC CGA AAC AAC GTA AAG GAT CCA				96
Gln Tyr Ser Ser Phe Val Asp Lys Ile Arg Asn Asn Val Lys Asp Pro	20	25	30	
AAC CTG AAA TAC GGT GGT ACC GAC ATA GCC GTG ATA GGC CCA CCT TCT				144
Asn Leu Lys Tyr Gly Gly Thr Asp Ile Ala Val Ile Gly Pro Pro Ser	35	40	45	
AAA GAA AAA TTC CTT AGA ATT AAT TTC CAA AGT TCC CGA GGA ACG GTC				192
Lys Glu Lys Phe Leu Arg Ile Asn Phe Gln Ser Ser Arg Gly Thr Val	50	55	60	
TCA CTT GGC CTA AAA CGC GAT AAC TTG TAT GTG GTC GCG TAT CTT GCA				240
Ser Leu Gly Leu Lys Arg Asp Asn Leu Tyr Val Val Ala Tyr Leu Ala	65	70	75	
ATG GAT AAC ACG AAT GTT AAT CGG GCA TAT TAC TTC AAA TCA GAA ATT				288
Met Asp Asn Thr Asn Val Asn Arg Ala Tyr Tyr Phe Lys Ser Glu Ile	80	85	90	95
ACT TCC GCC GAG TTA ACC GCC CTT TTC CCA GAG GCC ACA ACT GCA AAT				336
Thr Ser Ala Glu Leu Thr Ala Leu Phe Pro Glu Ala Thr Thr Ala Asn	100	105	110	
CAG AAA GCT TTA GAA TAC ACA GAA GAT TAT CAG TCG ATC GAA AAG AAT				384
Gln Lys Ala Leu Glu Tyr Thr Glu Asp Tyr Gln Ser Ile Glu Lys Asn	115	120	125	
GCC CAG ATA ACA CAG GGA GAT AAA AGT AGA AAA GAA CTC GGG TTG GGG				432
Ala Gln Ile Thr Gln Gly Asp Lys Ser Arg Lys Glu Leu Gly Leu Gly	130	135	140	
ATC GAC TTA CTT TTG ACG TTC ATG GAA GCA GTG AAC AAG AAG GCA CGT				480
Ile Asp Leu Leu Leu Thr Phe Met Glu Ala Val Asn Lys Lys Ala Arg	145	150	155	
GTG GTT AAA AAC GAA GCT AGG TTT CTG CTT ATC GCT ATT CAA ATG ACA				528
Val Val Lys Asn Glu Ala Arg Phe Leu Leu Ile Ala Ile Gln Met Thr	160	165	170	175
GCT GAG GTA GCA CGA TTT AGG TAC ATT CAA AAC TTG GTA ACT AAG AAC				576
Ala Glu Val Ala Arg Phe Arg Tyr Ile Gln Asn Leu Val Thr Lys Asn	180	185	190	
TTC CCC AAC AAG TTC GAC TCG GAT AAC AAG GTG ATT CAA TTT GAA GTC				624
Phe Pro Asn Lys Phe Asp Ser Asp Asn Lys Val Ile Gln Phe Glu Val	195	200	205	
AGC TGG CGT AAG ATT TCT ACG GCA ATA TAC GGG GAT GCC AAA AAC GGC				672
Ser Trp Arg Lys Il Ser Thr Ala Ile Tyr Gly Asp Ala Lys Asn Gly	210	215	220	
GTG TTT AAT AAA GAT TAT GAT TTC GGG TTT GGA AAA GTG AGG CAG GTG				720

161

Val	Phe	Asn	Lys	Asp	Tyr	Asp	Phe	Gly	Phe	Gly	Lys	Val	Arg	Gln	Val	
225						230					235					
AAG	GAC	TTG	CAA	ATG	GGA	CTC	CTT	ATG	TAT	TTG	GGC	AAA	CCA	AAG	GCC	768
Lys	Asp	Leu	Gln	Met	Gly	Leu	Leu	Met	Tyr	Leu	Gly	Lys	Pro	Lys	Ala	
240					245					250					255	
ATG	GGC	GGC	GGC	GGC	TCT	GCA	CCA	ATG	GCA	GAA	GGA	GGA	GGG	CAG	AAT	816
Met	Gly	Gly	Gly	Gly	Ser	Ala	Pro	Met	Ala	Glu	Gly	Gly	Gly	Gln	Asn	
				260					265					270		
CAT	CAC	GAA	GTG	GTG	AAG	TTC	ATG	GAT	GTC	TAT	CAG	CGC	AGC	TAC	TGC	864
His	His	Glu	Val	Val	Lys	Phe	Met	Asp	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	
			275					280					285			
CAT	CCA	ATC	GAG	ACC	CTG	GTG	GAC	ATC	TTC	CAG	GAG	TAC	CCT	GAT	GAG	912
His	Pro	Ile	Glu	Thr	Leu	Val	Asp	Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	
		290					295					300				
ATC	GAG	TAC	ATC	TTC	AAG	CCA	TCC	TGT	GTG	CCC	CTG	ATG	CGA	TGC	GGG	960
Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	
	305					310					315					
GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	GAG	TGT	GTG	CCC	ACT	GAG	GAG	TCC	1008
Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	
320					325				330						335	
AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	ATC	AAA	CCT	CAC	CAA	GGC	CAG	CAC	1056
Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	Ile	Lys	Pro	His	Gln	Gly	Gln	His	
				340					345					350		
ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	1104
Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	
			355					360					365			
AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	AAT	CCC	TGT	GGG	CCT	TGC	TCA	GAG	1152
Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	Asn	Pro	Cys	Gly	Pro	Cys	Ser	Glu	
		370					375					380				
CGG	AGA	AAG	CAT	TTG	TTT	GTA	CAA	GAT	CCG	CAG	ACG	TGT	AAA	TGT	TCC	1200
Arg	Arg	Lys	His	Leu	Phe	Val	Gln	Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	
		385				390					395					
TGC	AAA	AAC	ACA	GAC	TCG	CGT	TGC	AAG	GCG	AGG	CAG	CTT	GAG	TTA	AAC	1248
Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	
400					405				410					415		
GAA	CGT	ACT	TGC	AGA	TGT	GAC	AAG	CCG	AGG	CGG	GGC	GGC	GGC	GGC	TCT	1296
Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys	Pro	Arg	Arg	Gly	Gly	Gly	Gly	Ser	
				420					425					430		
GCC	ATG	GCA	CCA	ATG	GCA	GAA	GGA	GGA	GGG	CAG	AAT	CAT	CAC	GAA	GTG	1344
Ala	Met	Ala	Pro	Met	Ala	Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	
			435					440						445		

162

GTG AAG TTC ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG Val Lys Phe Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu 450 455 460	1392
ACC CTG GTG GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC Thr Leu Val Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile 465 470 475	1440
TTC AAG CCA TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT Phe Lys Pro Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn 480 485 490 495	1488
GAC GAG GGC CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG Asp Glu Gly Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met 500 505 510	1536
CAG ATT ATG CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG Gln Ile Met Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met 515 520 525	1584
AGC TTC CTA CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA Ser Phe Leu Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg 530 535 540	1632
GCA AGA CAA GAA AAT CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT Ala Arg Gln Glu Asn Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His 545 550 555	1680
TTG TTT GTA CAA GAT CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr 560 565 570 575	1728
GAC TCG CGT TGC AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys 580 585 590	1776
AGA TGT GAC AAG CCG AGG CGG TGATGAGTCG AC Arg Cys Asp Lys Pro Arg Arg 595	1809

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80

TGGTCCCAGGCTGCACCC ATGTGTGAAGGAGGAGGGCAGAATCAT

30

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81

ATG_ATT'CTGCCCTCCTCCTTCACACATG GGTGCAGCCTGGGACCA

30

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82

GCCAAGTGGTCCCAGG CTGCATGTCCCATGGCAGAAGG AGGAGGGCAG

30

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83

CTGCCCTCCTCCTTCTGCCATGGG ACATGCAGCCTGGGACCACTTGGC

30

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84

Ile Arg Val Arg Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85

Lys Arg Lys Arg Lys Lys
 1 5

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..455
- (D) OTHER INFORMATION: /product= "VEGF121 Cys +4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC      50
      Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala
          1              5              10

TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC ATG      98
Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met
      15              20              25

TGT GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG      146
Cys Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe Met

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165

30	35	40	45	
GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC				194
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp				
	50	55	60	
ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC				242
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser				
	65	70	75	
TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG				290
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu				
	80	85	90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG				338
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg				
	95	100	105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG				386
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln				
	110	115	120	125
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA				434
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu				
	130	135	140	
AAA TGT GAC AAG CCG AGG CGG TGATGACTGC AG				467
Lys Cys Asp Lys Pro Arg Arg				
	145			

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..587
- (D) OTHER INFORMATION: /product= "VEGF165 Cys +4"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC	50
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala	
1 5 10	
TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA CCC ATG	98

166

Leu	Leu	Leu	Tyr	Leu	His	His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	Pro	Met	
15						20					25					
TGT	GCA	GAA	GGA	GGA	GGG	CAG	AAT	CAT	CAC	GAA	GTG	GTG	AAG	TTC	ATG	146
Cys	Ala	Glu	Gly	Gly	Gly	Gln	Asn	His	His	Glu	Val	Val	Lys	Phe	Met	
30					35					40					45	
GAT	GTC	TAT	CAG	CGC	AGC	TAC	TGC	CAT	CCA	ATC	GAG	ACC	CTG	GTG	GAC	194
Asp	Val	Tyr	Gln	Arg	Ser	Tyr	Cys	His	Pro	Ile	Glu	Thr	Leu	Val	Asp	
				50					55					60		
ATC	TTC	CAG	GAG	TAC	CCT	GAT	GAG	ATC	GAG	TAC	ATC	TTC	AAG	CCA	TCC	242
Ile	Phe	Gln	Glu	Tyr	Pro	Asp	Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	Ser	
			65					70					75			
TGT	GTG	CCC	CTG	ATG	CGA	TGC	GGG	GGC	TGC	TGC	AAT	GAC	GAG	GGC	CTG	290
Cys	Val	Pro	Leu	Met	Arg	Cys	Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	Leu	
		80					85					90				
GAG	TGT	GTG	CCC	ACT	GAG	GAG	TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	CGG	338
Glu	Cys	Val	Pro	Thr	Glu	Glu	Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	Arg	
	95					100					105					
ATC	AAA	CCT	CAC	CAA	GGC	CAG	CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	CAG	386
Ile	Lys	Pro	His	Gln	Gly	Gln	His	Ile	Gly	Glu	Met	Ser	Phe	Leu	Gln	
110				115					120					125		
CAC	AAC	AAA	TGT	GAA	TGC	AGA	CCA	AAG	AAA	GAT	AGA	GCA	AGA	CAA	GAA	434
His	Asn	Lys	Cys	Glu	Cys	Arg	Pro	Lys	Lys	Asp	Arg	Ala	Arg	Gln	Glu	
				130					135					140		
AAT	CCC	TGT	GGG	CCT	TGC	TCA	GAG	CGG	AGA	AAG	CAT	TTG	TTT	GTA	CAA	482
Asn	Pro	Cys	Gly	Pro	Cys	Ser	Glu	Arg	Arg	Lys	His	Leu	Phe	Val	Gln	
			145					150					155			
GAT	CCG	CAG	ACG	TGT	AAA	TGT	TCC	TGC	AAA	AAC	ACA	GAC	TCG	CGT	TGC	530
Asp	Pro	Gln	Thr	Cys	Lys	Cys	Ser	Cys	Lys	Asn	Thr	Asp	Ser	Arg	Cys	
			160				165					170				
AAG	GCG	AGG	CAG	CTT	GAG	TTA	AAC	GAA	CGT	ACT	TGC	AGA	TGT	GAC	AAG	578
Lys	Ala	Arg	Gln	Leu	Glu	Leu	Asn	Glu	Arg	Thr	Cys	Arg	Cys	Asp	Lys	
			175			180					185					
CCG	AGG	CGG	TGATGACTGC	AG												599
Pro	Arg	Arg														
190																

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 13..456
 (D) OTHER INFORMATION: /product= "VEGF121 Cys+2 with NcoI sites"

(ix) FEATURE:

(A) NAME/KEY: misc_recomb
 (B) LOCATION: 1..6
 (D) OTHER INFORMATION: /note= "NcoI restriction site"

(ix) FEATURE:

(A) NAME/KEY: misc_recomb
 (B) LOCATION: 98..103
 (D) OTHER INFORMATION: /note= "NcoI restriction site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GGATCCGAAA CC ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT	48
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu	
1 5 10	
GCC TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA TGT	96
Ala Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Cys	
15 20 25	
CCC ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC	144
Pro Met Ala Glu Gly Gly Gly Gln Asn His His Glu Val Val Lys Phe	
30 35 40	
ATG GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG	192
Met Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val	
45 50 55 60	
GAC ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA	240
Asp Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro	
65 70 75	
TCC TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC	288
Ser Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly	
80 85 90	
CTG GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG	336
Leu Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met	
95 100 105	
CGG ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA	384
Arg Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu	
110 115 120	
CAG CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA	432

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Gln His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln
 125 130 135 140

GAA AAA TGT GAC AAG CCG AGG CGG
 Glu Lys Cys Asp Lys Pro Arg Arg
 145

456

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 599 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 12..587
- (D) OTHER INFORMATION: /product= "VEGF165 Cys+2 with NcoI sites"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 1..6
- (D) OTHER INFORMATION: /note= "NcoI restriction site"

(ix) FEATURE:

- (A) NAME/KEY: misc_recomb
- (B) LOCATION: 97..102
- (D) OTHER INFORMATION: /note= "NcoI restriction site"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GGATCCGAAA C ATG AAC TTT CTG CTG TCT TGG GTG CAT TGG AGC CTT GCC	50
Met Asn Phe Leu Leu Ser Trp Val His Trp Ser Leu Ala	
1 5 10	
TTG CTG CTC TAC CTC CAC CAT GCC AAG TGG TCC CAG GCT GCA TGT CCC	98
Leu Leu Leu Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Cys Pro	
15 20 25	
ATG GCA GAA GGA GGA GGG CAG AAT CAT CAC GAA GTG GTG AAG TTC ATG	146
Met Ala Glu Gly Gly Gly Gln Asn His His Val Val Lys Phe Met	
30 35 40 45	
GAT GTC TAT CAG CGC AGC TAC TGC CAT CCA ATC GAG ACC CTG GTG GAC	194
Asp Val Tyr Gln Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp	
50 55 60	
ATC TTC CAG GAG TAC CCT GAT GAG ATC GAG TAC ATC TTC AAG CCA TCC	242
Ile Phe Gln Glu Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser	

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65	70	75	
TGT GTG CCC CTG ATG CGA TGC GGG GGC TGC TGC AAT GAC GAG GGC CTG			290
Cys Val Pro Leu Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu			
80	85	90	
GAG TGT GTG CCC ACT GAG GAG TCC AAC ATC ACC ATG CAG ATT ATG CGG			338
Glu Cys Val Pro Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg			
95	100	105	
ATC AAA CCT CAC CAA GGC CAG CAC ATA GGA GAG ATG AGC TTC CTA CAG			386
Ile Lys Pro His Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln			
110	115	120	125
CAC AAC AAA TGT GAA TGC AGA CCA AAG AAA GAT AGA GCA AGA CAA GAA			434
His Asn Lys Cys Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu			
130	135	140	
AAT CCC TGT GGG CCT TGC TCA GAG CGG AGA AAG CAT TTG TTT GTA CAA			482
Asn Pro Cys Gly Pro Cys Ser Glu Arg Lys His Leu Phe Val Gln			
145	150	155	
GAT CCG CAG ACG TGT AAA TGT TCC TGC AAA AAC ACA GAC TCG CGT TGC			530
Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys			
160	165	170	
AAG GCG AGG CAG CTT GAG TTA AAC GAA CGT ACT TGC AGA TGT GAC AAG			578
Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys Arg Cys Asp Lys			
175	180	185	
CCG AGG CGG TGATGACTGC AG			599
Pro Arg Arg			
190			

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..7
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90

Pro Lys Lys Arg Lys Val Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..8
 - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:91

Pro Pro Lys Lys Ala Arg Glu Val
1 5

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..9
 - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92

Pro Ala Ala Lys Arg Val Lys Leu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..5
 - (D) OTHER INFORMATION: /product= nuclear translocation sequence
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93

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Lys Arg Pro Arg Pro

1 5

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..5
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94

Lys Ile Pro Ile Lys

1 5

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95

Gly Lys Arg Lys Arg Lys Ser

1 5

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96

Ser Lys Arg Val Ala Lys Arg Lys leu
1 5

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..9
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97

Ser His Trp Lys Gln Lys Arg Lys Phe
1 5

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..8
- (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98

Pro Leu Leu Lys Lys Ile Lys Gln
1 5

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..7

(D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99

Pro Gln Pro Lys Lys Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:100

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..15

(D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100

Pro Gly Lys Arg Lys Lys Glu Met Thr Lys Gln Lys Glu Val Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 12 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..12

(D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101

Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Ala Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:102:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..7
 - (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102

Asn Tyr Lys Lys Pro Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..7
 - (D) OTHER INFORMATION: /product= nuclear translocation sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103

His Phe Lys Asp Pro Lys Arg
1 5

Claims

We claim:

1. A conjugate, comprising a targeted agent and a vascular endothelial cell growth factor (VEGF) polypeptide or a portion thereof, wherein the conjugate binds to a VEGF receptor resulting in internalization of the linked targeted agent.
2. A conjugate comprising the following components: $(\text{VEGF})_n$, $(\text{L})_q$ and $(\text{targeted agent})_m$, wherein:
 - L is a linker;
 - VEGF is a VEGF monomer or a portion thereof;
 - at least one VEGF monomer is linked at any residue via $(\text{L})_q$ to at least one targeted agent;
 - m and n, which are selected independently, are at least 1;
 - q is 0 or more as long as the resulting conjugate binds to the targeted receptor is internalized and delivers the targeted agent; and
 - the conjugate binds to a receptor that interacts with and internalizes VEGF, whereby the targeted agent(s) is internalized in a cell bearing the receptor.
3. The conjugate of claim 2, wherein m and n, which are selected independently, are 1-6.
4. The conjugate of claim 2, wherein n is 1.
5. The conjugate of claim 4, wherein m is 1.
6. The conjugate of claim 2, wherein q is 1.
7. The conjugate of claim 2, wherein L is selected from the group consisting of protease substrates, linkers that increase the flexibility of the conjugate, linkers that increase the solubility of the conjugate, photocleavable linkers and acid cleavable linkers.
8. A conjugate of any one of claims 1 or 2, wherein a VEGF polypeptide is selected from the group consisting of VEGF₁₂₁, VEGF₁₂₀, VEGF₁₈₈, VEGF₁₈₉, VEGF₁₆₄, VEGF₁₆₅, VEGF₂₀₅, VEGF₂₀₆ and a modified VEGF₁₂₁, VEGF₁₂₀, VEGF₁₈₈, VEGF₁₈₉, VEGF₁₆₄, VEGF₁₆₅, VEGF₂₀₅ or VEGF₂₀₆ in which a cysteine

residue is added or replaces a non-essential amino acid residue within about 20 amino acids of the N-terminus or C-terminus of the monomer.

9. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a cytotoxic agent.

10. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a ribosome-inactivating protein.

11. The conjugate of claim 10, wherein the targeted agent is a saporin.

12. The conjugate of any one of claims 1 or 2, wherein the targeted agent is a nucleic acid.

13. The conjugate of any one of claims 1 or 2, wherein the targeted agent is an antisense nucleic acid.

14. The conjugate of claim 2, wherein the conjugate is a fusion protein selected from the group consisting of FPSV1, FPSV2, FPSV3, FPSV4, FPSV5, FPSV6, FPSV7, FPSV8, FPSVV1, FPSVV2, FPSVV3, FPSVV4, FPSVV5, FPSVV6, FPSVV7 and FPSVV8.

15. The conjugate of claim 2 that has the formula:
targeted agent-(L)_q-VEGF-(L)_r-VEGF, wherein
q and r, which may be the same or different, are 0 or 1.

16. A conjugate that has the formula:
(targeted agent)_m-(L)_q-(VEGF)_n, wherein
L is a linker;
VEGF is a VEGF monomer or a portion thereof;
at least one VEGF monomer is linked at any residue via (L)_q to at least one
targeted agent;
m and n, which are selected independently, are at least 1;
q is 0 or more as long as the resulting conjugate binds to the targeted receptor
is internalized and delivers the targeted agent; and

the conjugate binds to a receptor that interacts with and internalizes VEGF, whereby the targeted agent(s) is internalized in a cell bearing the receptor.

17. The conjugate of any one of claims 1-16, for use as an active therapeutic substance.

18. The conjugate of any one of claims 1-16, for use in the manufacture of a medicament for treating a VEGF-mediated pathophysiological condition.

19. The conjugate of claim 18, wherein the pathophysiological condition is a dermatological disorder with underlying vascular proliferation, a solid tumor, or an ophthalmic disorder of the hyperproliferating blood vessels of the retina, iris, conjunctiva or vitreous humor.

20. The conjugate of any one of claims 1-16, for inhibiting proliferation of cells bearing VEGF receptors.

21. The conjugate of claim 12, for effecting gene therapy, wherein the conjugate includes a nuclear translocation sequence operatively linked to the targeted nucleic acid or VEGF.

22. A DNA fragment comprising a sequence of nucleotides encoding the conjugate of any one of claims 1-6 and 8-16.

23. A plasmid, comprising the DNA of claim 22.

24. A plasmid of claim 23, wherein the plasmid is an expression vector for expression of the DNA encoding the conjugate in eukaryotic cells or is an expression vector for expression of the conjugate in prokaryotic cells.

25. The plasmid of claim 24, wherein the vector is pP_L-λ.

26. A plasmid of claim 23, selected from the group consisting of PZ72B1, PZ73B1, PZ74B1, PZ74F5, PZ75B1, PZ75F5, PZ76B1, PZ76F5, PZ77B1, PZ78F5, PZ79B1, PZ79F5, PZ80B1, PZ81B1, PZ81F5, PZ82B1, PZ83B1, PZ84B1, PZ85B1, PZ85F5, PZ86B1, PZ95B1, PZ96B1, PZ97B1, PZ98B1, PZ99B1, PZ100B1, PZ101B1.

PZ102B1, PZ103B1, PZ104B1, PZ105B1, PZ106I1, PZ107I1, PZ108I1, PZ109J1, PZ110J1, PZ111J1, PZ112J1, PZ113J1 and PZ114J1.

27. A cell transfected or transformed with the expression vector of claim 24.

28. The cell of claim 27 that is a bacterial cell.

29. A method of producing a conjugate of any one of claims 1-6 and 8-16, comprising culturing the cells of claim 27 under conditions whereby DNA is transcribed and translated to produce the conjugate.

30. A vascular endothelial cell growth factor monomer that is modified by insertion of a cysteine residue within about twenty amino acids of the N-terminus or C-terminus, wherein the inserted residue replaces a nonessential residue in the unmodified VEGF monomer or is added to the VEGF monomer.

31. The modified monomer of claim 30, wherein the cysteine residue is inserted within about 20 residues of the N-terminus.

32. The VEGF monomer of claim 46 that is VEGF CYS+4, VEGF CYS+2, or VEGF CYS-1.

33. DNA encoding the VEGF monomer of claim 30.

34. A pharmaceutical composition, comprising the conjugate of any one of claims 1-16, in combination with a physiologically acceptable excipient.

35. A method of producing a VEGF fusion protein comprising:

(a) culturing cells transformed with a plasmid comprising $pP_L-\lambda$, containing a DNA fragment according to claim 22, under conditions whereby the DNA fragment is transcribed and translated;

(b) lysing the cells to release inclusion bodies;

(c) solubilizing the inclusion bodies in a denaturant; and

(d) removing the denaturant, thereby refolding the fusion protein.

36. A method of producing VEGF, comprising:

- (a) culturing cells transformed with a plasmid comprising pP_L-λ containing a DNA fragment encoding VEGF, under conditions whereby the DNA fragment is transcribed and translated;
- (b) lysing the cells to release inclusion bodies;
- (c) solubilizing the inclusion bodies in a denaturant; and
- (d) removing the denaturant, thereby refolding the fusion protein.

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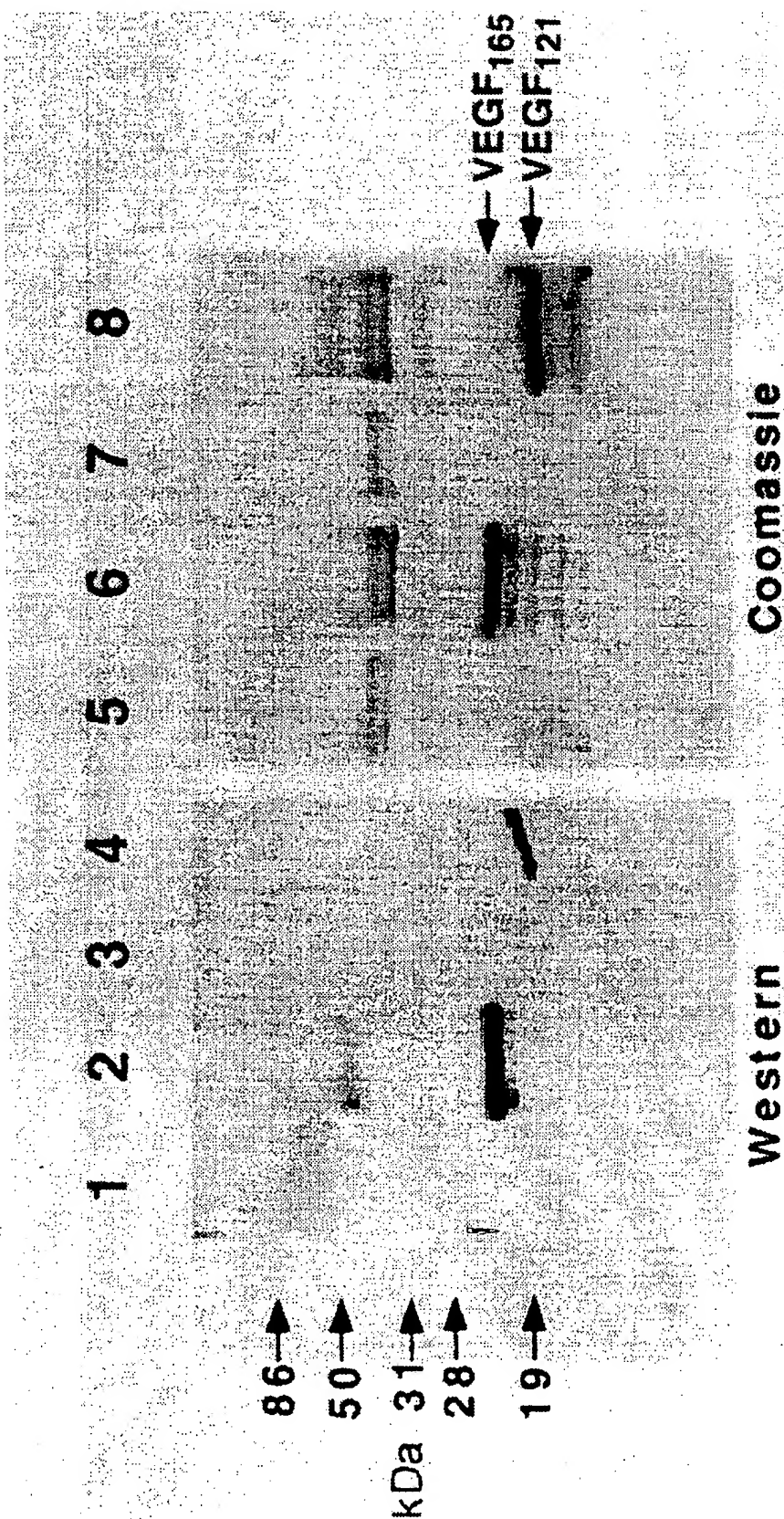


FIG. 1

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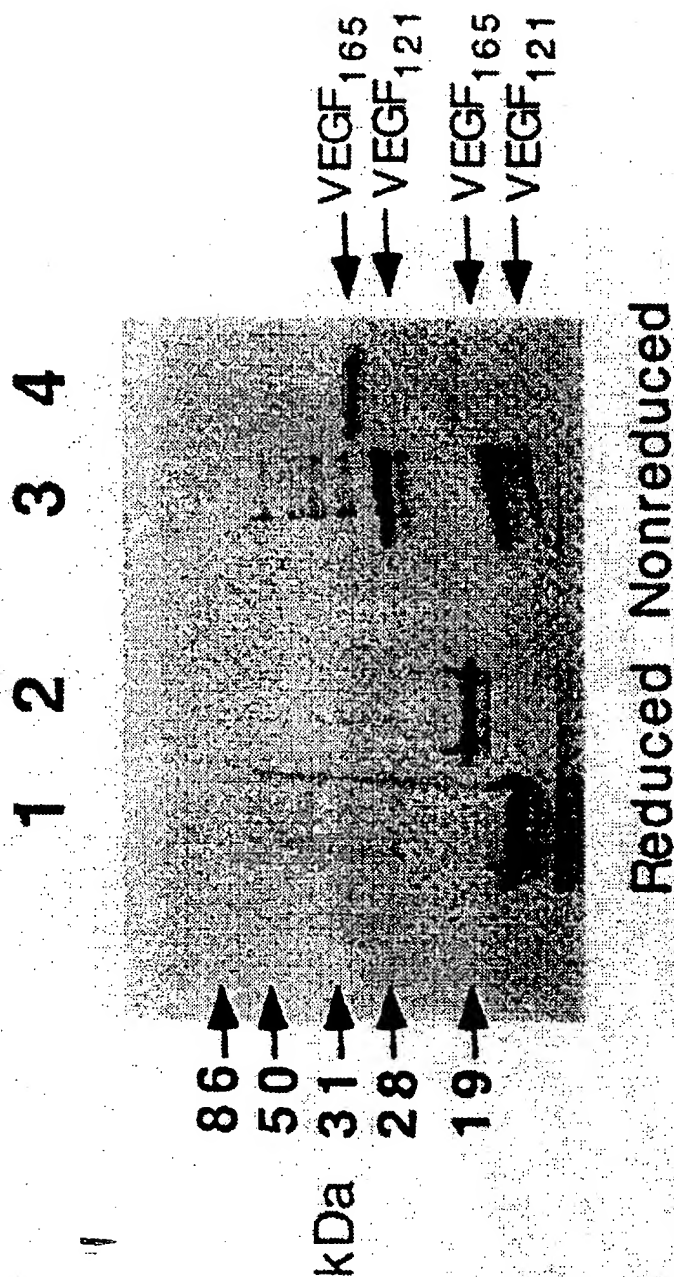
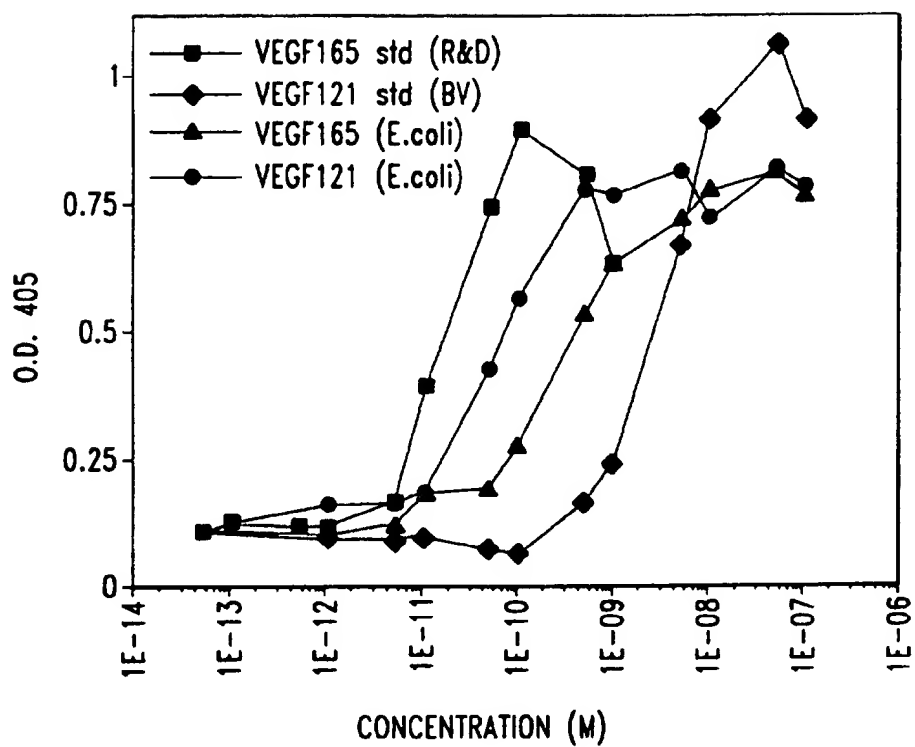


FIG. 2

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*Fig. 3*

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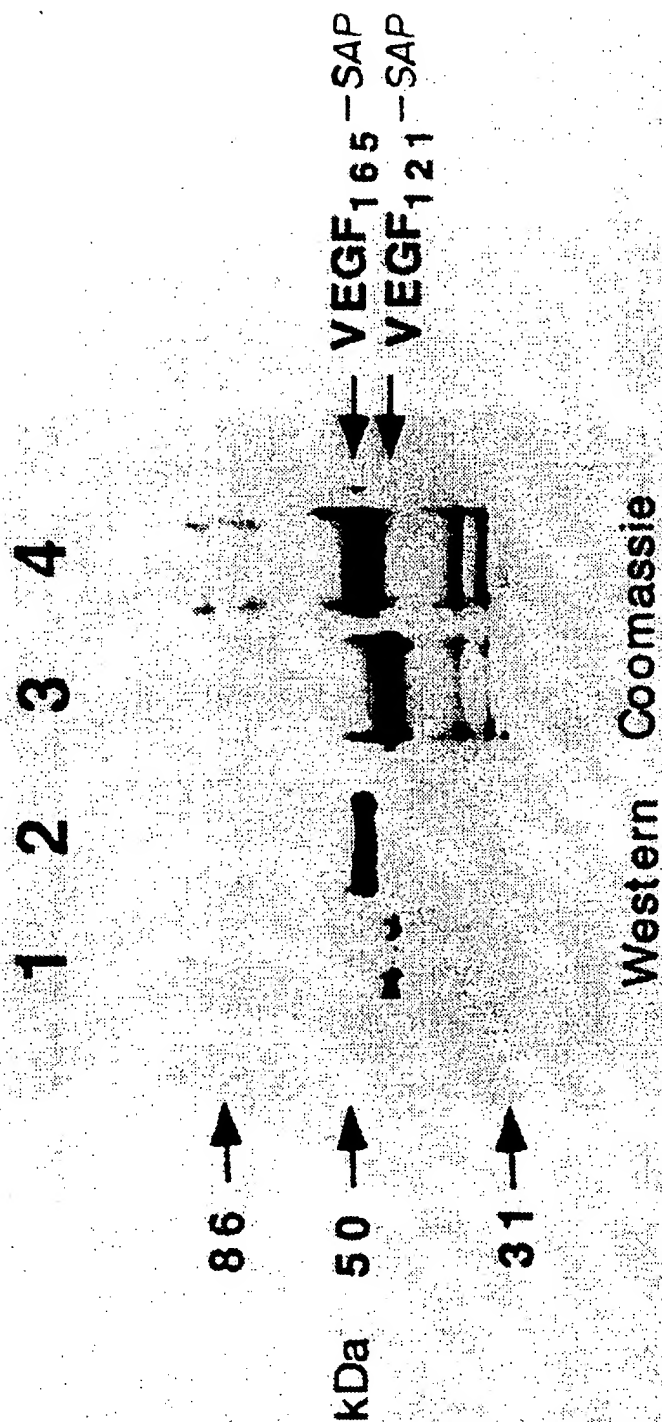


FIG. 4

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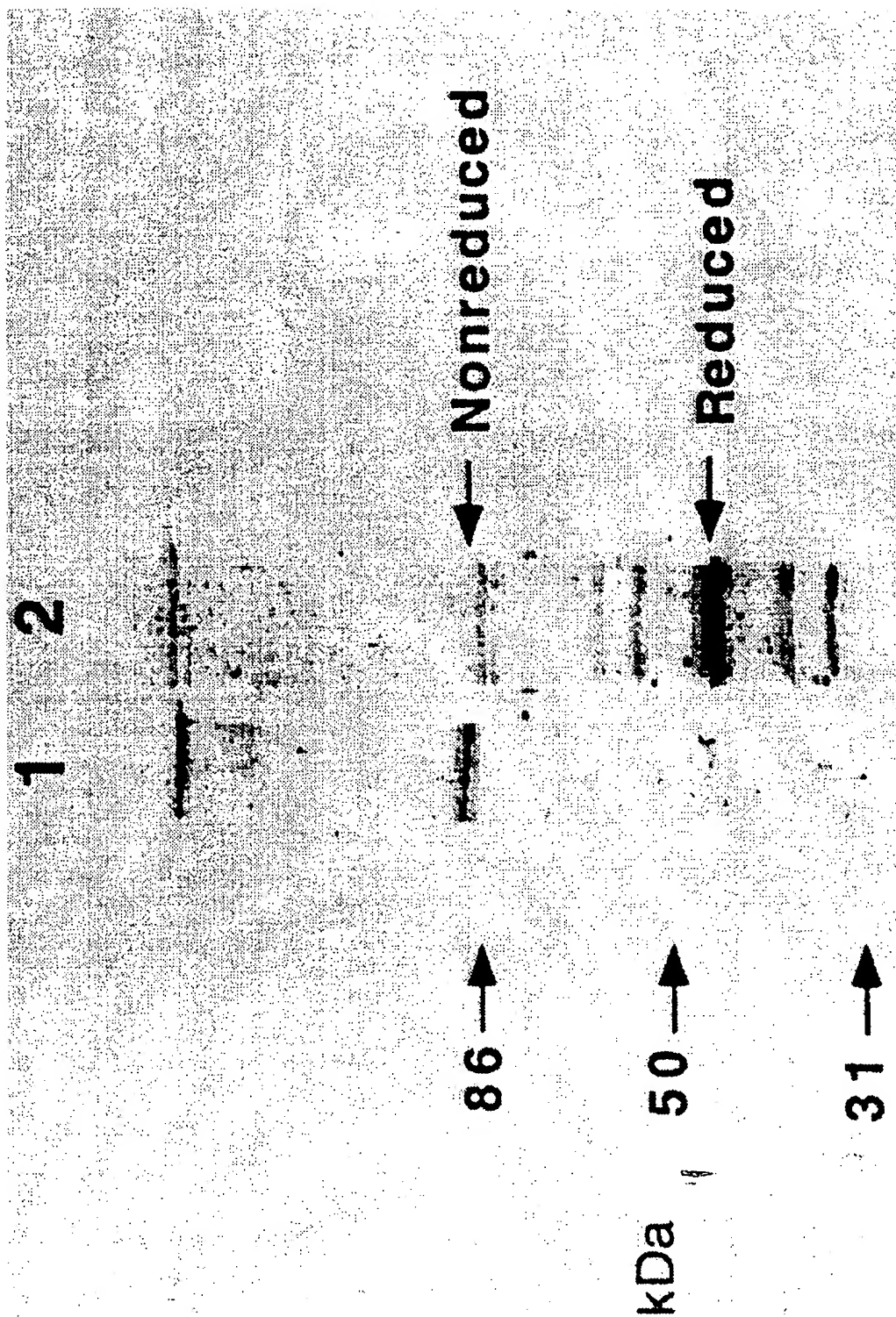
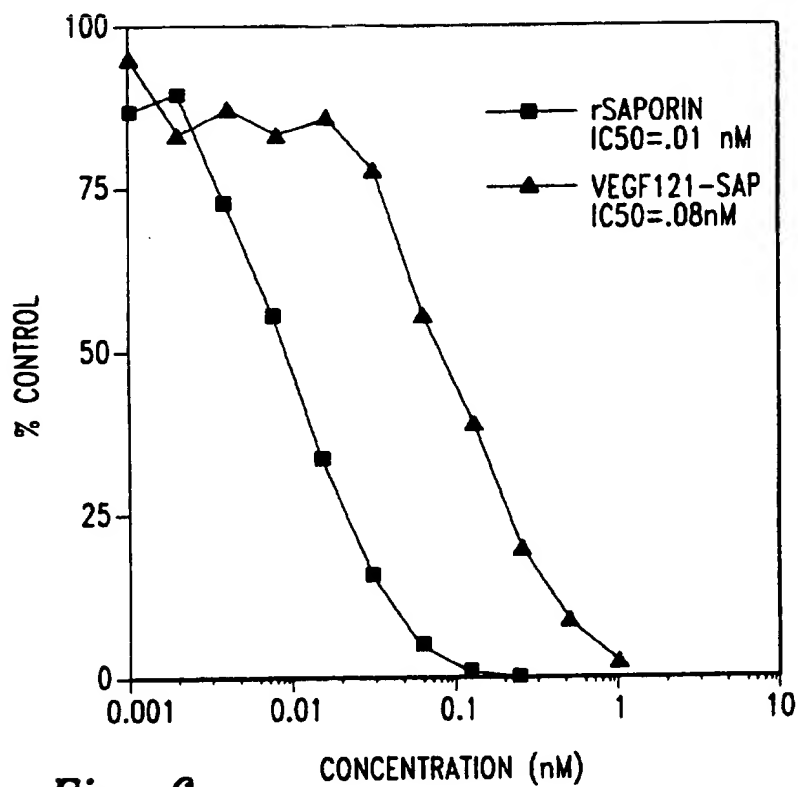
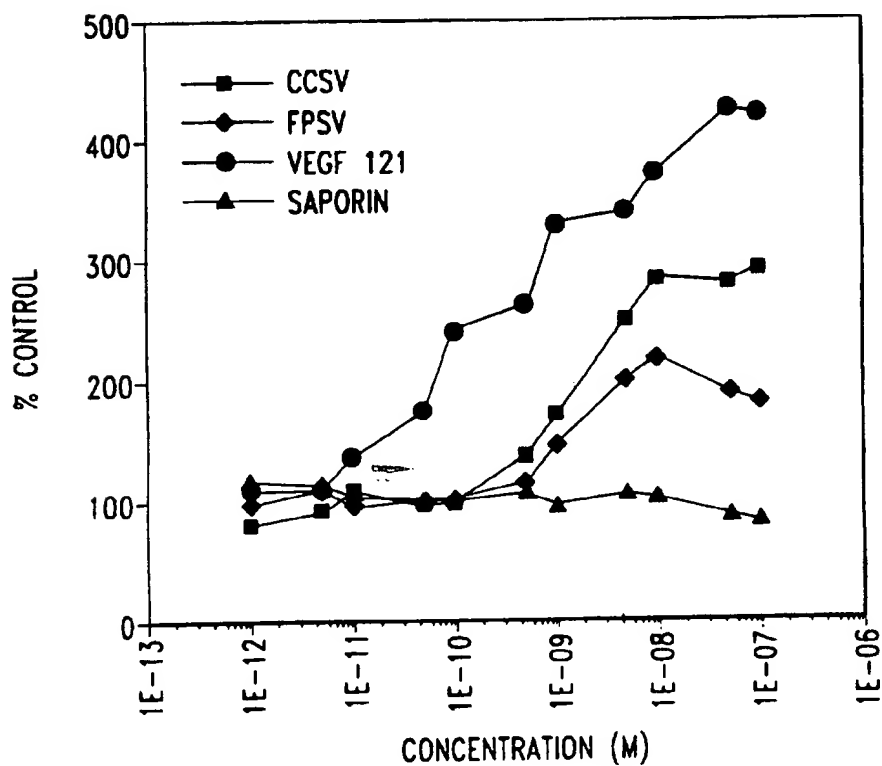


FIG. 5

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*Fig. 6**Fig. 7*

INTERNATIONAL SEARCH REPORT

International application No

PCT/US 95/10973

A. CLASSIFICATION OF SUBJECT MATTER
IPC 6 A61K47/48 A61K41/00 C07K14/475 C07K19/00 C12N15/62
C12N15/12 C12N1/21

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 6 A61K C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO,A,93 25688 (WHITTIER INST FOR DIABETES AND ;PRIZM PHARMACEUTICALS INC (US); LA) 23 December 1993 cited in the application see page 5, line 3 - line 30 see page 7, line 22 - line 27	1-36
X	see page 15, line 10 - line 13; claims; examples	1-36
P,X	--- WO,A,95 03831 (PRIZM PHARMA INC ;WHITTIER INST FOR DIABETES AND (US)) 9 February 1995 see claims	1
Y	--- WO,A,94 10202 (GENENTECH INC) 11 May 1994 see page 9, line 8 - line 24	1-36
X	see page 9, line 32 - line 37 see page 14, line 24 - line 30 ---	30-33,36
	-/--	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

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- * O* document referring to an oral disclosure, use, exhibition or other means
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- * T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- * X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- * Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- * &* document member of the same patent family

Date of the actual completion of the international search

19 December 1995

Date of mailing of the international search report

12.02.96

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Fax (+ 31-70) 340-3016

Authorized officer

BERTE, M

INTERNATIONAL SEARCH REPORT

International Application No.
PCT/US 95/10973

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO,A,90 13649 (GENENTECH INC) 15 November 1990 see claims; example IV; table 1 ---	30-36
Y	WO,A,92 11872 (SALK INST FOR BIOLOGICAL STUDI ;US GOVERNMENT (US)) 23 July 1992 see claims 1,3,4,8 ---	1-36
A	WO,A,91 02058 (CALIFORNIA BIOTECHNOLOGY INC) 21 February 1991 see page 8, line 34 - line 38; claims 1,25 ---	30-33,36
P,X	DATABASE BIOSIS BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US AN=95:186713 see abstract & 86TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, TORONTO, ONTARIO, CANADA & PROCEEDINGS OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH ANNUAL MEETING, vol.36, no.0, page 424 VICTOR K.D. ET AL. 'CHARACTERIZATION OF HUMAN VASCULAR ENDOTHELIAL GROWTH FACTOR MITOTOXINS.' ---	1-36
A	CHEMICAL ABSTRACTS, vol. 120, no. 25, 20 June 1994, Columbus, Ohio, US; abstract no. 316874, YANG, YADONG ET AL 'Cloning of cDNA for human VEGF and its high-efficiency expression in E. coli' see abstract & GAOJISHU TONGXUN (1993), 3(5), 13-16 CODEN: GTONE8;ISSN: 1002-0470, ---	22-28
P,X	DATABASE MEDLINE US NATIONAL LIBRARY OF MEDICINE (NLM), BETHESDA, MD, US AN=95110840 cited in the application see abstract & BIOCHEM. BIOPHYS. ACTA, vol.1246, no.1, 5 January 1995 pages 1 - 9 CLAFFEY K.P. ET AL. 'STRUCTURAL REQUIREMENTS FOR DIMERIZATION, GLYCOLISATION, SECRETION, AND BIOLOGICAL FUNCTION OF VPf/VEGF.' ---	30-33

-/--

INTERNATIONAL SEARCH REPORT

Internat. Application No
PCT/US 95/10973

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A,P	JOURNAL OF BIOLOGICAL CHEMISTRY, vol.269, no.52, , MD US pages 32879 - 32885 ANDY J. G. PÖTGENS, ET AL. 'COVALENT DIMERIZATION OF VASCULAR PERMEABILITY FACTOR /VASCULAR ENDOTHELIAL GROWTH FACTOR IS ESSENTIAL FOR ITS BIOLOGICAL ACTIVITY. EVIDENCE FROM CYS TOR SER MUTATIONS.' see page 32879	30-33
P,X	--- DATABASE BIOSIS BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US 95:186644 see abstract & 86TH ANNUAL MEETING OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH, 18 March 1995, TORONTO, ONTARIO, CANADA & PROCEEDINGS OF THE AMERICAN ASSOCIATION FOR CANCER RESEARCH ANNUAL MEETING, vol.36, no.0, page 413 THIERRY A.R. ET AL. 'IN VITRO AND IN VIVO INHIBITION OF TUMORIGENICITY OF NEOPLASTIC KAPOSÍ'S SARCOMA CELL LINE (KS Y-1) BY LIPOSOMAL IL-6, IL-8 AND VEGF ANTISENSE OLIGONUCLEOTIDES.'	1-13, 17-20,34
A	--- BIOCONJUGATE CHEMISTRY, vol.3, , WASHINGTON US pages 375 - 381 M. WESTBY ET AL. 'PREPARATION AND CHARACTERIZATION OF RECOMBINANT PRORICIN CONTAINING AN ALTERNATIVE PROTEASE-SENSITIVE LINKER SEQUENCE.' cited in the application see page 375	1,2,7
E	--- WO,A,95 24928 (PRIZM PHARMA INC) 21 September 1995 see page 25, line 32 - page 28, line 32; claims -----	

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US 95/ 10973

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
please see enclosed sheet!
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/210

INCOMPLETE SEARCH OR MEANINGFUL SEARCH NOT POSSIBLE

2. Obscurities, Inconsistencies,...

In view of the large number of compounds which are defined by the general definition of claim 1,2,14 and dependent claims and also in view of the definition of products by means of their biological, chemical and/or pharmacological properties, the search had to be restricted for economic reasons.

The search was limited to the compounds for which pharmacological data was given and/or the compounds mentioned in the examples (see guidelines, Part B, Chapter III, paragraph 3.6)

Partially searched claims: 1-7,9,15,22,23,30,33,34

INTERNATIONAL SEARCH REPORT

Information on patent family members

Internat Application No
PCT/US 95/10973

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
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